

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2004, 01:16:04 ; Search time 511 Seconds
(without alignments)
3649.824 Million cell updates/sec

Title: US-09-964-277-21

Perfect score: 517

Sequence: 1 MLPLSLQTVFSLYFWNWR.....LKVGSQSSFGSMEIIIVS 517

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2353733 seqs, 1803733377 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4700994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
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-DB=Published Applications NA -QWTF=fastap -SUFFIX=olip2n.rnnp -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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Alignment Scores:					
Pred. No.:	0				Length: 3332
Score:	517.00				Matches: 517
Percent Similarity:	100.00%				Conservative: 0
Best Local Similarity:	100.00%				Mismatches: 0

ALIGNMENTS

RESULT 1
US-09-964-277-20
; Sequence 20, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 3332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-20

Alignment Scores:					
Pred. No.:	0				Length: 3332
Score:	517.00				Matches: 517
Percent Similarity:	100.00%				Conservative: 0
Best Local Similarity:	100.00%				Mismatches: 0

Sequence 20, Appl
Sequence 3, Appl
Sequence 27, Appl
Sequence 673, App
Sequence 1, Appl
Sequence 1, Appl
Sequence 25, Appl
Sequence 26234, A
Sequence 255, App
Sequence 257, App
Sequence 2429, App
Sequence 8120, Ap
Sequence 1, Appl
Sequence 463, App
Sequence 1817, A
Sequence 18617, A
Sequence 8068, App
Sequence 31436, A
Sequence 3118, Ap
Sequence 3, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 11, Appl
Sequence 654, App
Sequence 270, App
Sequence 1135, Ap
Sequence 183, App
Sequence 4, Appl
Sequence 48, Appl
Sequence 1, Appl
Sequence 69, Appl
Sequence 330, App
Sequence 12, Appl
Sequence 18, Appl
Sequence 241, App
Sequence 15, Appl
Sequence 16818, A
Sequence 310, App
Sequence 310, App
Sequence 310, App
Sequence 310, App
Sequence 310, App

Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-964-277-21 (1-517) x US-09-964-277-20 (1-3332)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
 DB 842 ATGTTGGCTCTCTCTCTTCCAGACTGTTTCTCACTGACTGTTGGGTAACTGGAGAGA 901

QY 21 AlaserThrLeuPheThrCysLeuGlnGluMetGlnGlnGlnGlyTyrVal 40
 DB 902 GCITCAACTCTGTTCACTCTGCTGAGGAGCTGATGACAGAGATGGGATGTTATGTG 961

QY 41 LeuAsnAlaserAsnThrCysProLysProAspPheLeuProGluSerHisPheLeuArg 60
 DB 962 TTAATGCCAGCAATACCTGTCCAAAGCCTGACATTATCCCGAGTCTCATTTCTGCTG 1021

QY 61 ValProValAsnAspSerPheCysGluLysIleLeuProTrpLeuAspLysSerValAsp 80
 DB 1022 GTGCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCGTGGTGGCAAAATCAGTAGAT 1081

QY 81 PheIleGluLysAlaLysAlaserAsnGlyCysValLeuValHisCysLeuAlaGlyIle 100
 DB 1082 TTCAATGAGAAAGCAAAAGCCTCAATGGATGTGTTCTAGTGCACTGTGTTAGCTGGATC 1141

QY 101 SerArgSerAlaThrIleAlaIleAlaIleAlaIleAlaIleMetLysArgMetAspMetSerLeuAsp 120
 DB 1142 TCCGCTCCGCCACCTCGTATCGCTACATCATGAAGAGGATGGACATGCTTTAGAT 1201

QY 121 GluAlaTyrArgPheValLysGluLysArgProThrIleSerProAsnPheAsnPheLeu 140
 DB 1202 GAAGCTTACAGATTTGTGAAAGAAAGAAAGACCTACTATCTCAACTTTCATTTTCTG 1261

QY 141 GlyIleLeuLeuAspTyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLys 160
 DB 1262 GGCCAACTCTCGACTATGAGAAGAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAG 1321

QY 161 SerLysLysLeuLeuIleLysGluLysProAsnGluProValProAlaValSerGlu 180
 DB 1322 AGCAACTCAAGCTGTGCACTTGAGAGAGCAAAATGAACCTGTGCTGCTGCTCAGAG 1381

QY 181 GlyGlyLysSerGluThrProLeuSerProCysAlaAspSerAlaThrSerGlu 200
 DB 1382 GGTGGACAGAAAG 1441

QY 201 AlaAlaGlyGlnArgProValHisProAlaSerValProSerValProSerValGlnPro 220
 DB 1442 GCACAGAGCAAGAGCCCGTGTATCCGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAG 1501

QY 221 SerLeuLeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAsp 240
 DB 1502 TCGTGTGTAGAGAGACAGCCCGCTGTGTACAGCGCTCAAGTGGCTGCACCTGTCCGAGAC 1561

QY 241 ArgLeuGluAspSerAsnLysLysLysArgSerPheSerLeuAspIleLysSerValSer 260
 DB 1562 AGGTGGAGACAGCAATAGCTCAAGCTTCTCTCTGATATCAAAATCAGTTTCA 1621

QY 261 TyrSerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGlu 280
 DB 1622 TATTCAAGCAGATGGAG 1681

QY 281 TyrTyrLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProVal 300
 DB 1682 TACTACAACTTCCACTACTCTGGATGGAGCAACCAAGCTATGCCAGTGTCTCCCTGTT 1741

QY 301 GlnGluLeuSerGlnGlnThrProGluThrSerProAspLysGlnGluAlaSerIlePro 320
 DB 1742 CAGAACTATCGAG 1801

QY 321 LysLysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHisSerValArg 340
 DB 1802 AAGAAGTGACAGCCCGAGGCTTTCAGACAGCCAGAGCAAGGATGTCATTCGTGTCAGA 1861

341 ThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySer 360
 DB 1862 ACCAGCAGCAGTGGCACCCGAGAGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGC 1921

QY 361 ValGluLeuAspLeuThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeu 380
 DB 1922 GTGGAGGAGCAATTAACACACAGCTTCTCTTTGGGCTTTTCCACAGCCAGACACCTC 1981

QY 381 ThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThr 400
 DB 1982 ACAGAGTCTGTGGCTGGGCTTAAGGGCTGGCACTGGATATCTTTGGCCCCCAGACC 2041

QY 401 SerThrProSerLeuThrSerSerTrpPheAlaThrGluSerSerHisPheThrSer 420
 DB 2042 TCTACCTCTTCCCTGACACAGCTGTGTATTTTGGCCAGAGTCTCTACACTTCTCTCT 2101

QY 421 AlaserAlaIleTyrGlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuPro 440
 DB 2102 GCTCAGCCTATCTACGGAGCAGTGCCTACTTCTGCTTACAGTGGCAGCAGCTGCC 2161

QY 441 ThrCysGlyAspGlnValTyrSerValArgArgArgGlnLysProSerAspArgAlaAsp 460
 DB 2162 ACTTGGCGAGACCAAGTCTATTCTGTGCGCAGCGCAGAGCAAGCAAGTGCAGAGCTGAC 2221

QY 461 SerArgArgSerTrpHisGluSerProPheGluLysGlnPheLysArgArgSerCys 480
 DB 2222 TCGCGCGGAGCTGGCATGAGAGAGACCCCTTTGAAAAGCAGTTTAAACGACAGAGTGC 2281

QY 481 GlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArgGluLeuGlyLys 500
 DB 2282 CAATATGGAATTTGGAGAGAGCATCATGTCCAGAGAACAGGTCCACGGAGAGAGCTGGGAAA 2341

QY 501 ValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 517
 DB 2342 GTGGSCAGTCACTAGCTTTTTCGGSCACATGGAATCATTTAGGTCTCC 2392

RESULT 2
 US-09-816-494-3
 ; Sequence 3, Application US/09816494
 ; Patent No. US20020034807A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel A.
 ; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
 ; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 10448-030002
 ; CURRENT APPLICATION NUMBER: US/09/816,494
 ; CURRENT FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 60/191,858
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1998
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-816-494-3

Alignment Scores:
 Pred. No.: 0 Length: 1998
 Score: 488.00 Matches: 488
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.39% Indels: 0
 DB: 9 Gaps: 0

US-09-964-277-21 (1-517) x US-09-816-494-3 (1-1998)

QY 30 GlnLeuMetGlnGlnGlnGlnGlyTyrValLeuAsnAlaserAsnThrCysProLys 49
 DB 532 GAGCTGTATGACAGAGATGGATGTTATGTGTAAATGCGAGCAATACCTGTGCCAAG 591

QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69

Db 592 CTTGACTTTATCCCGAGTCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGTGAG 651
Qy 70 LysIleLeuProTrrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
Db 652 AAAATTTTGGCGTGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAA 711
Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 712 GGATGTGTTCTAGTGACACTGTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATGCC 771
Qy 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 772 TACATCATGAGAGGATGACATGCTCTTTAGATGAAGCTTACATGTTGTGAAGAAAAA 831
Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 832 AGACCTACTATATCTCCAAACTTCAATTTCTGGGCCAACTCTCTGGGACTATGAGAAAG 891
Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu 169
Db 892 ATTAAGACCAGACTGGAGCATCAGGGCCAAAGACAACTCAAGCTGCTGCACCTGGAG 951
Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
Db 952 AAGCCAAATGAACCTGCTCTCTCAGAGGGTGGACAGAAAGCAGAGCGCCCTC 1011
Qy 190 SerProProCysAlaAspSerAlaThrSerGluAlaIleGlyGlnArgProValHisPro 209
Db 1012 AGTCACCTCTGGCGATCTGCTACCTCAGAGGAGCAGACAAAGCCGCTGATCCC 1071
Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1072 GCCAGCGTGCCAGCGTGCCAGCGTGCCAGCGTGGCTGTTAGAGGACAGCCCGCTGGTA 1131
Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1132 CAGGCGCTCAGTGGGCTGCACCTGTCGCCAGACAGCTGGAGACACAAATAGCTCAAG 1191
Qy 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
Db 1192 CGTCTCTCTCTCGATATCAATCAGTTTCATATTCAGCCAGCATGGCGCATCTCTA 1251
Qy 270 HisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1252 CATGGCTTCTCTCATGAGAAGATCTTTGGAATACTACAAACCTTCCACTCTGAT 1311
Qy 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1312 GGGACCAACAGCTATGCGAGTTCTCCCTGTTTCAGGACTATCGAGCAGACTCCCGAA 1371
Qy 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1372 ACCAGTCTGTATAGGAGGAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCA 1431
Qy 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
Db 1432 GACAGCCAGCAAGCATGATTCGATTCGATCAGAACCCAGCAGCAGTGGCCCGCCAGG 1491
Qy 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 1492 TCCCTTTTATCTCCACTGCATCGAAGTGGAGCGGTGGAGGACAATTACACACAGCTTC 1551
Qy 370 LeuPheGlyLeuSerThrSerGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 1552 CTTTTCGGGCTTTCCACAGCCAGCAGCACCTCAGAACTGCTGGCTTGGGCTTTAAG 1611
Qy 390 GlyTrrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrr 409
Db 1612 GGTGGCACTCGGATATCTTGGCCCCCAGACCTTACCTCTCCCTGACACGAGCTGG 1671
Qy 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysAla 429
Db 1672 TATTTTGGCCAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTGC 1731

Qy 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 1732 AGTTACTCTGCTACAGCTGCAGCAGCTGCCCACTTGCAGAGACCAAGTCTATTCTGTG 1791
Qy 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgSerTrrHisGluGluSer 469
Db 1792 CGCAGCGCGCAGAGCCACCAAGTGCAGAGAGCTTCTCGCGCGGAGCTGGCATGAGAGAGC 1851
Qy 470 ProPheGluLysGlnPheLysArgLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 1852 CCGTTGAAAAGCAGTTTAAACGCGAGAAGCTGCCAAATGGAAATTTGGAGAGAGCATCATG 1911
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 1912 TCAGAGAACAGCTCACGGGAGAGCTGGGAAAGTGGGAGTGGCAGTCTAGCTTTTCGGGC 1971
Qy 510 SerMetGluIleIleGluValSer 517
Db 1972 AGCATGGAAATCATTTAGGTTCTCC 1995

RESULT 3

US-10-377-072-27
Sequence 27, Application US/10377072
Publication No. US20040009501A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Miyoung
APPLICANT: Tsai, Pong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MPI03-018OMNIM
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:

Pred. No.: 0 Length: 1398
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 15 Gaps: 0

US-09-964-277-21 (1-517) x US-10-377-072-27 (1-1998)

Qy 30 GluLeuMetGlnGlnAenGlyIleGlyTyValLeuAsnAlaSerAsnThrCysProlys 49
Db 532 GAGCTGATGAGCAGATGGATGGTATGTGTAAATGCCAGCAATACCTGTCCAAAG 591
Qy 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 592 CCTGACTTATCCCGAGTCTCATTTCCCTGCGTGTGCTGTGAATGACAGCTTTTGTGAG 651
Qy 70 LysIleLeuProIrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
Db 652 ARAATTTTGGTGGTGGCAAAATCAGTAGATTTCAATTCAGAAAGCAAAAGCCTCCAAAT 711
Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 712 GGATGTCTTCTAGTGCACCTGTTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC 771
Qy 110 TyIleMetLysArgMetAspMetSerLeuAspGluAlaTyArgPheValLysGluLys 129
Db 772 TACATCATGAAGAGATGGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAANA 831
Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrgLysLys 149
Db 832 AGACCTACTATATCTCAAACTTCAATTTCTGGGCCAACTCCTGGACTATGAGAAGAAG 891
Qy 150 IleLysGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu 169
Db 892 ATTAAGAACCCAGACTGAGCATCAGGGCCCAAGAGCAAACTCAAGCTGCTGCACCTGGAG 951
Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
Db 952 ARGCCAAATGAACTGCTCCCTGCTGTCTCAGAGGTGGACAGAAAGCGAGCGCCCTC 1011
Qy 190 SerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
Db 1012 AGTCCACCTGTGCGCACTCTGCTACTCAGAGSCAGCAGGCAAAAGGCCCGCTGCATCCC 1071
Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1072 GCCAGCTGCCAGCGTGCACCGTGCAGCGTGCCTGCTGTTAGAGGACAGCCCGCTGGTA 1131
Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1132 CAGCGCTCAGTGGCTGCACCTGTCCGACAGCAGGCTGGAAGACAGCAATAAGCTCAAG 1191
Qy 250 ArgSerPheSerLeuAspLysSerValSerTyArgSerAlaSerMetAlaAlaSerLeu 269
Db 1192 CGTTCCTCTCTCTGGATATCAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTA 1251
Qy 270 HisGlyPheSerSerGluAspAlaLeuGluTyTyLysProSerThrThrLeuAsp 289
Db 1252 CATGGCTTCTCCATCAGAGATGCTTTGGATATCTACAACTTCCACTACTCTGGAT 1311
Qy 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluSerGluGlnThrProGlu 309
Db 1312 GGGACCAACAGCTATGCCAGTCTCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAA 1371
Qy 310 ThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1372 ACCAGTCTGATAGGAGGAGGAGCAGCATCCCAAGAGCTGCAGACCCCGAGGCTTCA 1431
Qy 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
Db 1432 GACAGCCAGACGAGCGATTTGCTTGGTTCAGAACCCAGCAGCAGTGGCACCAGGAGG 1491

Qy 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyHisThrSerPhe 369
Db 1492 TCCCTTTTATCTCCACTGTCGAAGTGGAGCGTGGAGGACAAATTACACACAGCTTC 1551
Qy 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 1552 CTTTTCGGCTTTTCCACGACGACGACCTCAGAACTCTGTGGCTGGGCTTAAG 1611
Qy 390 GlyThrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTip 409
Db 1612 GGTGGCACTCGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACACAGCTGG 1671
Qy 410 TyPheAlaThrGluSerSerHisPheTySerAlaSerAlaIleTyGlyGlySerAla 429
Db 1672 TATTTTGGCAGAGAGTCTCTCACCTTCTACTCTGCTCAGCCATCTACGAGGAGCTGCC 1731
Qy 430 SerTySerAlaTySerCysSerGlnLeuProThrCysGlyAspGlnValTySerVal 449
Db 1732 AGTTACTCTGCTACAGCTGCAGCCAGCTGCCACTTTCGGAGACCAAGTCTATTCTGTG 1791
Qy 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
Db 1792 CGCAGCGCCGCAAGCCAAAGTGACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGAGC 1851
Qy 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 1852 CCTTTGAAAGACAGTTTAAAGCCAGAGCTGCCAAATGGAAATTTGGAGAGCATCATG 1911
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 1912 TCAGAGAACAGCTCAGCGGAGAGCTGGGGAAGTGGGCGAGTCACTAGTCTAGCTTTTCGGGC 1971
Qy 510 SerMetGluIleIleLeuValSer 517
Db 1972 AGCATGGAATCATTTGAGGTCTCC 1995

RESULT 4

US-10-094-749-673
; Sequence 673, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAL, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 673
; LENGTH: 2102
; TYPE: DNA

QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
DB 1153 CTGACTTATCCCGAGTCATCTTCTGCGTGTGCGTGTGATGACAGCTTTGTGAG 1212
QY 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
DB 1213 AAAATTTTCCCGTGTGTGACAAATCAGTAGATTTCATTGAGAAGCAAAAGCTCCAAAT 1272
QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
DB 1273 GGATGTGTTCTAGTGCACCTGTTTACCTGGGATCTCCGCTCCGCCACCATCGCTATCGCC 1332
QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
DB 1333 TACATCATGAAGAGATGGACATGTCTTTAGATGAAGCTTACAGATTGTGGAAGAAAAA 1392
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
DB 1393 AGACCTACTATATCTCCAACTTCATTTCTGGGCCAACTCCTGGACTATGAGAAGAAG 1452
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
DB 1453 ATTAGAACCAGATGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAG 1512
QY 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
DB 1513 AAGCCAAATGAACCTGTCTCTGCTGTCTCAGAGGTGACAGAAAGAGGAGCGCCCTC 1572
QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
DB 1573 AGTCCACCTGTGCGGACTCTGCTACCTCAGAGGCGAGGACAAAGGCCCGCTCATCCC 1632
QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
DB 1633 GCAGCGTGCACCGCTGCTCCAGCGTGCAGCGTGCCTGTTAGAGGAGCGCCCTGGTA 1692
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
DB 1693 CAGCGCTCAGTGGGCTGCACCTGTCCGACAGACAGGCTGGAAGACAGCAATAAGCTCAAG 1752
QY 250 ArgSerPheSerLeuAspLysSerValSerTyrSerAlaSerMetAlaAspSerLeu 269
DB 1753 CGTTCTCTCTCTGATATCAAAATCAGTTTCATATTGAGCGAGTGGCAGCATCTTTA 1812
QY 270 HisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
DB 1813 CATGGCTTCTCTCATCAGAGATGCTTTGGATATCTACAAACCTTCCACTACTCTGAT 1872
QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
DB 1873 GGGACCAACAAGCTATGCCAGTTCTCCCTGTTCAGGAACCTATCGGAGCAGACTCCGAA 1932
QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
DB 1933 ACCAGTCTCTGATGAAGAGGAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCA 1992
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
DB 1993 GACAGCCAGAGCAAGCGATTGCTATTCGTTGAGTCCAGAACCCAGCAGCAGTGGCAGCCAGAGG 2052
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
DB 2053 TCCCTTTTATCTCCATGCAATCGAAGTGGAGCGTGGAGGACATATACACACAGCTTC 2112
QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLys 389
DB 2113 CTTTTGGGCTTTCCACCGCCAGCAGCACCTTCAGAGTCTGCTGGCTGGGCTTAAG 2172
QY 390 GlyTrpHisSerAspIleAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
DB 2173 GGCTGGCAGCTCGGATATCTTGGCCCCCAGACCTTACCTTCCCTTCCAGCAGAGCTGG 2232
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlySerAla 429

DB 2233 TATTTTGCACAGAGTCTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGCAGTGCC 2292
QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
DB 2293 AGTTACTCTGCTACAGCTGACCCAGCTGCCACATTCGGAGACCAAGCTATTCTGTG 2352
QY 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgSerTrpHisGluGluSer 469
DB 2353 CGCAGGCGCAGAAAGCCCAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGC 2412
QY 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
DB 2413 CCCITTTGAAGCAGTTTAAACGCAAGAGCTGCCAATGGAATTTGGAGAGACATCATG 2472
QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
DB 2473 TCAGAGAACAGCTCACGGAAGAGCTCGGGAAGAGTGGGAGTGCAGTCTAGCTTTTCGGGC 2532
QY 510 SerMetGluIleIleGluValSer 517
DB 2533 AGCATGGAATCATTTAGGTCTCC 2556
RESULT 6
US-09-816-494-1
; Sequence 1. Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1
Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 9 Gaps: 0
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DB 1120 GAGCTGATGCAGCAAGTGGGATTTGTTATGTGTAAATGCCAGCAATACCTGTCCAAAG 1179
QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
DB 1180 CTGACTTTATCCCGAGTCTCATTTCTCGTGTGCTGTGCTGTGATGACAGCTTTGTGAG 1239
QY 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
DB 1240 AAAATTTTCCCGTGTGTGACAAATCAGTAGATTTCATTGAGAAGCAAAAGCTCCAAAT 1299
QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
DB 1300 GGATGTGTTCTAGTGCATGTTTACTGGGATCTCCGCTCCGCCACCATCGCTATCGCC 1359

QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
DB 1360 TACATCATGAAGAGATGGACATCTCTTTAGATGAAGCTTACAGATTGTGAAAGAAAA 1419
QY 130 ArgProThrIleSerProAspPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
DB 1420 AGACTTACTATATCTCCAACTTCAATTTCTGGCCAACTCTCTGGACTATGAGAAGAG 1479
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLeuLysLeuGlu 169
DB 1480 ATTAAGAACCAAGATGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTGGAG 1539
QY 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
DB 1540 AAGCCAAATGAACCTGCTCCCTGCTGTCTCAGAGGCTGCAGAAAGCGAGAGCCCTTC 1599
QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaGlyGlnArgProValHisPro 209
DB 1600 AGTCACCCCTGTGCGACTCTGCTACCTCAGAGCGAGCAGCAAAAGCCCGTGCATCC 1659
QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuAspSerProLeuVal 229
DB 1660 GCCAGCGTGGCCAGCGTCCAGCGTGCAGCGCTGCTGTGTAGAGGACACCCCGCTGGTA 1719
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
DB 1720 CAGGCGCTCAGTGGCTGACCTGTCCGAGACAGGCTGGAGACAGCAATAAGCTCAAG 1779
QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
DB 1780 CGTTCCTCTCTCTGGATATCAAAATCATGTTTCAATTCAGCCAGCATGGCAGCATCTTA 1839
QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
DB 1840 CATGCTTCTCTCTCATCAGAGAGCTTTGGAACTACAAACCTTCCACTCTCTGGAT 1899
QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
DB 1900 GCGACCAACAGCTATGCGAGTCTCCCTCTTCCAGGAATCTATCGGAGCAGACTCCCGAA 1959
QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
DB 1960 ACCAGTCTGTATGAGAGAGAGCAGCATCCCAAGAGCTGCAGACCGCAGCGCTTCA 2019
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
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QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
DB 2080 TCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGCAATACCAACACAGCTTC 2139
QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuLys 389
DB 2140 CTTTTCGGCTTTCACACGACGACGACCTCAGAGTCTGTGGCTGGCGCTTAAG 2199
QY 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerTrp 409
DB 2200 GGCTGGCACTCGATATCTTGCCCCCAGACCTCTACCCCTTCCCTGACCGAGCGTGG 2259
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
DB 2260 TATTTTGGCACAGAGTCTTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2319
QY 430 SerTrpSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
DB 2320 AGTTACTTCTCTCAGCTGACGCGAGCTGCCACTTGCAGAGCAACCAAGTCTATTCTGTG 2379
QY 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
DB 2380 CGCAGCGCGCAAGCGCAAGTACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGC 2439
QY 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489

DB 2440 CCCTTTGAAAAGCAGTTTAAACCGAGAGCTGCAATGGAATTTGGAGAGCATCATG 2499
QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
DB 2500 TCAGAGAACAGGTCACGGGAAGAGCTGGGGAAGAGTGGGGAAGAGTGGGAGTCTAGCTTTTCGGGC 2559
QY 510 SerMetGluIleIleGluValSer 517
DB 2560 AGCATGGAATCATTTGAGTCTCC 2583
RESULT 7
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP103-0180NM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2586)
US-10-377-072-25
Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 15 Gaps: 0
US-09-964-277-21 (1-517) x US-10-377-072-25 (1-3544)

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Qy 50 ProAspPheileProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 1180 CTTGACTTATCCCGAGTCTCATTTCCGCGTGGCTGTGAATGACAGCTTTTGTGAG 1239
Qy 70 LysileLeuProTribLeuAspLysSerValAspPheileGluLysAlaLysAlaSerAsn 89
Db 1240 AAAATTTTCCGCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCAAAT 1299
Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 1300 GGAATGTTCTAGTGACACTGTTAGCTGGGATCTCCCGCTCGCCACCATCGCTATCGCC 1359
Qy 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 1360 TACATCATGAGAGGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAAGAAAA 1419
Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysIlys 149
Db 1420 AGACCTACTATATCTCAAACTTCAATTTTCTGGCCAACTCTCGACTATGAGAAGAAG 1479
Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLeuLysLeuLeuHisLeuGlu 169
Db 1480 ATTAGAACCAAGACTGGAGCATCAGGGCCAAAGACAACTCAAGCTCTGCACCTGGAG 1539
Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
Db 1540 AAGCCAAATGAACCTCTCCCTGCTGTCTCAGAGGGTGGACAGAAAGGAGAGCGCCCTC 1599
Qy 190 SerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
Db 1600 AGTCCACCTGTGCCACTCTGCTACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1659
Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1660 GCCAGCGTGGCCAGCTGCCAGCTGACGCTGACGCTGCTGTTAGAGACAGCGCGCTGTA 1719
Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1720 CAGCGCTCAGTGGGCTGACCTGTCCGAGACAGGCTGGAGACAGCAATTAAGCTCAAG 1779
Qy 250 ArgSerPheSerLeuAspLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
Db 1780 CGTTCCTCTCTCGATATCAATCAGTTTCATATTCAGCCAGCATGGCAGATCTTTA 1839
Qy 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1840 CATGGCTTCTCCTCATCAGAAGATGTTTGGAAATACACAAACCTTCCACTACTCTGGAT 1899
Qy 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1900 GGGACCAACAGCTATGCCAGTTCTCCCTGTTCAGGAATATTCGGAGCAGACTCCCGAA 1959
Qy 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1960 ACCAGTCTCTAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2019
Qy 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
Db 2020 GACAGCCAGAGCAGCGATTTGCTATTTGGTCAGAACCCAGGAGGAGGAGGAGGAGGAGG 2079
Qy 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 2080 TCCCTTTTATCTCCACTGCTATCGAAGTGGAGCGTGGAGGAGCAAAATACACACAGCTTC 2139
Qy 370 LeuPheGlyLeuSerThrSerGlnHisLeuThrLysSerAlaGlyLeuGlyLysLys 389
Db 2140 CTTTTCGGCTTTCCACAGCCAGCAGCAGCTCAGGAAGTCTGCTGGCTGGGCTTTAAG 2199
Qy 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409

Db 2200 GCGTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGAGCTGG 2259
Qy 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
Db 2260 TATTTTGCACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTSCC 2319
Qy 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2320 AGTTACTCTGCTCAGCTGACCCAGCTGCCACTTGGCGAGACCAAGTCTATTTCTGTG 2379
Qy 450 ArgAspArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
Db 2380 CCGACGGCGGAGAGCCAGTGCAGAGCTGACTCGCGGGAGCTGCATGATGAGAGAGC 2439
Qy 470 PropheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2440 CCGTTTGAAGACAGTCTTAAACGCGAGAGCTGCCAAATGGAAATTTGGAGAGCATCATG 2499
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2500 TCAGAGAACAGGTTCAGGAGAGCTGGGAGAGTGGGAGTCACTCTAGCTTTTCGGGC 2559
Qy 510 SerMetGluIleleGluValSer 517
Db 2560 AGCATGGAATCATTCAGGTCTCC 2583
RESULT 8
US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication NO. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234
Alignment Scores:
Pred. No.: 0 Length: 3625
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 12 Gaps: 0
US-09-964-277-21 (1-517) x US-10-425-114-26234 (1-3625)
Qy 30 GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
Db 1223 GAGCTCATGCAGCAGAAATGGGATGGTATGTTGTTAAATGCAGCAATACCTGTCCAAAG 1282
Qy 50 ProAspPheileProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 1283 CTTGACTTATCCCGAGTCTCATTTCCGCGTGGCTGTGAATGACAGCTTTTGTGAG 1342
Qy 70 LysileLeuProTribLeuAspLysSerValAspPheileGluLysAlaLysAlaSerAsn 89
Db 1343 AAAATTTTCCGCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCAAAT 1402

QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 1403 GGATGCTGTCTAGTGCATCTGTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC 1462
QY 110 TyrIleMetLysArgMetCaspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 1463 TACATCATGAAGAGATGGACATGTCCTTAGATGAAGCTTACAGATTGTGAAGAAGAAA 1522
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 1523 AGACCTACTATATCTCCAACTTCAATTTTCTGGCCAACTCTCTGGACTATGAGAAGAAG 1582
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLysLeuLeuHisLeuGlu 169
Db 1583 ATTAAGAACCAAGATGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTCACCTGGAG 1642
QY 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
Db 1643 AAGCCAAATGAACCTGCTCCCTGCTCTCAGAGGTTGGACAGAAAAGCGAGACGCCCTC 1702
QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
Db 1703 AGTCCACCTGTGGCGACTCTCTGCTACCTCAGAGGAGCAGCAAGAGCCGCTGCATCC 1762
QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1763 GCCAGCTGCCAGGTCGCCAGGTCGAGCGCTGCTGCTTTAGAGGACGCCCGCTGGTA 1822
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1823 CAGGCGCTCAGTGGCTGCACCTCTCCGACAGAGGCTGGAAGACAGCAATAAGCTCAAG 1882
QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
Db 1883 CGTTCCTCTCTGGATATCAATCATCATCTTCAATTCAGCCAGCATGGCAGCATCTTA 1942
QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1943 CATGCTTCTCTCATCAGAAGATGCTTTGGAACTACTACAACTCCACTACTCTGGAT 2002
QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 2003 GGGACCAACAAGCTATGCCAGTCTCCCTCTGTTCCAGAACTATCGGAGCAGATCCCGAA 2062
QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 2063 ACCAGTCTCTATAGGAGAAAGCAGCATCCCAAGAGCTGCAGACCGCCAGCTTCA 2122
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
Db 2123 CACAGCCAGAGCAAGCGATTGCAATTCGTCAGAAACCAAGCAGCAGTGCCACCGCCAGAG 2182
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
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QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 2243 CTTTTCGGCTTTCACACAGCAGCAGCAGCATCCAGAACTGCTGCTGGCCCTTAAG 2302
QY 390 GlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
Db 2303 GGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGGACAGCAGCTGG 2362
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
Db 2363 TATTTTGGCAGAGTCTCTACATTTCTACTCTGCTCAGCCATCTACGAGCAGCATGCC 2422
QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2423 AGTTACTTGCCTACAGCTCAGCGCAGCTGCCCCACTTGGCAGCAACCAAGTCTATTCTGTG 2482

QY 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
Db 2483 CGCAGGGCGCAGAAAGCCAACTGACAGAGCTGACTCGCGCGAGCTGGCATGAAAGAGAGC 2542
QY 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2543 CCGTTTGAAGAAGCAGTTTAAACGCAGAGCTGCCAATGGAAATTTGGAGAGACATCATG 2602
QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2603 TCAGAGAACAGCTCACGGGAAGAGCTGGGAAAAGTGGCAGTCAGTCTAGCTTTTCGGGC 2662
QY 510 SerNetGluIleIleGluValSer 517
Db 2663 AGCATGGAATCATTTAGGTTCTCC 2686
RESULT 9
US-10-072-012-255
; Sequence 255, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 2200

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-255

Alignment Scores:
Pred. No.: 0 Length: 2200
Score: 408.00 Matches: 435
Percent Similarity: 99.32% Conservative: 0
Best Local Similarity: 99.32% Mismatches: 3
Query Match: 78.92% Indels: 0
DB: 12 Gaps: 0

US-09-964-277-21 (1-517) x US-10-072-012-255 (1-2200)

QY 83 GluLeuAlaLysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArg 102
Db 793 GAGAAAGCAAAAGCCCTCCAAATGATGTCTAGTGCACCTGTTAGCTGGGATCTCCCGC 852
QY 103 SerAlaThrIleAlaIleAlaTyrlleMetLysArgMetAspMetSerLeuAspGluAla 122
Db 853 TCCGCCACCATCCCTATCGCTACATCATGAAGAGGATGGACATGCTTTAGATGAAGCT 912
QY 123 Tyr---ArgPheValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGly 141
Db 913 TACAGGAGATTGTGAAGAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGC 972
QY 142 GluLeuLeuAspTyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSer 161
Db 973 CAACCTCTGGACTATGAGAAGAGAGATTAAAGAACCAAGACTGGAGCATCAGGCCCAGAGC 1032
QY 162 LysLeuLysLeuLeuHisLeuGluLysProAsnGluProValProAlaValSerGluGly 181
Db 1033 AAACCTCAAGCTGTGCACCTGGAGAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGT 1092
QY 182 GlyGlnLysSerGluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAla 201
Db 1093 GGACAGAAAAGCAGAGCGCCCTCACTCAGCCCTGTGCCACTCTGTCTACCTCAGAGCA 1152
QY 202 AlaGlyGlnArgProValHisProAlaSerValProSerValProSerValGlnProSer 221
Db 1153 GCAGGACAAAGCCCGGTGCATCCCGCAGCGGTGCCAGCGTCCAGCGGTGCAGCGCTG 1212
QY 222 LeuLeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArg 241
Db 1213 CTGTTAGAGCAGACCGCGCTGTGTACAGCGCTCAGTGGCGTGCACCTGTCCGACACAGG 1272
QY 242 LeuGluAspSerHisLysLysLysArgSerPheSerLeuAspIleLysSerValSerTyr 261
Db 1273 CTGGAAGACGCAATAAGCTCAAGCGTTCCTCTCTCTGGATATCAATCAGTTTCATAT 1332
QY 262 SerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyr 281
Db 1333 TCAGCCAGCATGGCAGCATCTTTACATGGCTTCTCTCATCAGAAAGATGCTTTGGAATAC 1392
QY 282 TyrLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGln 301
Db 1393 TACAAACCTTCCACTACTCTGGATGGAGCAACAAGCTATGCGAGTTCCTCCCTGTTTCA 1452
QY 302 GluLeuSerGluGlnThrProGluThrSerProAspLysGluGluAlaSerIleProLys 321
Db 1453 GAACCTTCGGAGCAGACTCCGAAACCGTCTGATAGAGGAGGAGCAGCATCCCCAAG 1512
QY 322 LysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThr 341
Db 1513 AAGTTCGAGACCGCCAGCGCTTCAGACGACGAGCAAGCGATTGCAATTCGGTCCAGAAC 1572
QY 342 SerSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerVal 361
Db 1573 AGCAGCAGTGCACCGCCAGAGGTCCCTTTATCTCCATGTCATCGAAGTGGAGCGTG 1632
QY 362 GluAspSerThrHisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThr 381
Db 1633 GAGGACAAATACCAACACAGCAGCTTCCTTTTCGGCGTTTCCACCAGCCAGCAGCCTCAG 1692
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RESULT 10

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US-10-072-012-257
; Sequence 257, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Bsha
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
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;; PRIOR APPLICATION NUMBER: 60/266,767
;; PRIOR FILING DATE: 2001-02-05
;; PRIOR APPLICATION NUMBER: 60/267,057
;; PRIOR FILING DATE: 2001-02-07
;; PRIOR APPLICATION NUMBER: 60/266,975
;; PRIOR FILING DATE: 2001-02-07
;; PRIOR APPLICATION NUMBER: 60/267,459
;; PRIOR FILING DATE: 2001-02-08
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1391
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 257
;; LENGTH: 2071
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-072-012-257

Alignment Scores:

Pred. No.: 7,166-297 Length: 2071
Score: 304.00 Matches: 483
Percent Similarity: 98.98% Conservative: 0
Best Local Similarity: 98.98% Mismatches: 5
Query Match: 98.80% Indels: 5
DB: 12 Gaps: 0

US-09-964-277-21 (1-517) x US-10-072-012-257 (1-2071)

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QY 30 GluLeuMetGlnGlnAsnGlyLeuGlyTyrValLeuAsnAlaSerThrCysProLys 49
DB 592 GAGCTGATGCGAGCAATGGGATGGTATGTATGTTAAATCCAGCAATACCTGTCARAG 651
QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
DB 652 CTGACTTATCCCGAGTCTCATTTCTCGCTGCTGCTGTAATGACACTTTTGTGAG 711
QY 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaSerAsn 89
DB 712 AAAATTTTGGCGGTGTTGGCAAAATCATGATGATTTCATTGAGAAGCAAAAGCCTCCAA 771
QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
DB 772 GGATGTTTCTAGTGCACTGTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC 831
QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
DB 832 TACATCATGAAGAGATGGACATGCTTTTACATGAAGCTTACAGATTGTGAAAGAAAA 891
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
DB 892 AGACCTACTATATCTCCAAACTTCATTTTCTGGGCCAACTCTCTGGACTATGAGAAGAG 951
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
DB 952 ATTAAGAACCAAGACTGGAGCATCAGGGCAAGAGCAAACTCAAGCTGTGCACTGGAG 1011
QY 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
DB 1012 AGCCAAATGAACCTGCTCCCTGCTCTCAGAGGTGACAGAAAAGCGAGACGCCCTC 1071
QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaGlyGlnArgProValHisPro 209
DB 1072 AGTCACCTGTGCGGACTGCTTACCTCAGAGCAGCAGCAAAAGCGCGGTGCATC-- 1129
QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
DB 1130 C--C--G--CC--AGCGTACCCAGCGTGGCGCTGCTGTTAGAGGACAGCCCGCTGGTA 1182
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
DB 1183 CAGGGGCTCAGTGGGCTGCACCTGTCCGACACAGGCTGGAGACAGCAATAGCTCAAG 1242
QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
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DB 1243 CGTTCCTTCTCTCGGATATCAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTA 1302
QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
DB 1303 CATGGCTTCTCTCATCAGAAAGATGCTTTGGAAATACATAAAACCTTCCACTACTCTGGAT 1362
QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
DB 1363 GGGACCAACAGCTATCCAGTTCTCCCTGTTTCAGAACTATCGGAGCAGACTCCCGAA 1422
QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
DB 1423 ACCAGTCTGATAGGAGGAAGCAGCATCCCAAGAAGCTGCAGACCCGAGCCCTTCA 1482
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
DB 1483 GACAGCCAGAGCAGCGATTCGATTCGTCAGAACCCAGCAGCAGTGGCCGCCAGAGG 1542
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
DB 1543 TCCCTTTTATCTCCACTGTCATCGAAGTGGAGCGTGGAGCAATTACCACACAGCTTC 1602
QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuLys 389
DB 1603 CTTTTCGGCTTTCCACCAGCCAGCACCTCACAGAGTCTGCTGGCTGGGCCCTTAAG 1662
QY 390 GlyThrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTip 409
DB 1663 GGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGG 1722
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
DB 1723 TATTTTCCACAGAGTCTCCACACTTCTACTCTGCTCAGCCATCTACGAGGAGCAGTGCC 1782
QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
DB 1783 AGTTACTCTGCTTACAGCTGCAGCCAGCTGCCCACTTGGGAGACCAAGTCTATTCTGTG 1842
QY 450 ArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
DB 1843 CGCAGCGCGCAGAAAGCCAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGC 1902
QY 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
DB 1903 CCCTTTGAAGAGCAGTTTAAACCGCAGAGCTGCCAATGGAAATTTGGAGAGCATCATG 1962
QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
DB 1963 TCAGAGAACAGGTCACGGGAAGAGCTGGGGAAGTGGGAGTGGCAGTCAGTCTAGCTTTTCGGGC 2022
QY 510 SerMetGluIleIleGluValSer 517
DB 2023 AGCATGGAAATCATTTGAGGTCTCC 2046
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RESULT 11

US-10-108-260A-2429
; Sequence 2429, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2429
; LENGTH: 1916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2429

Alignment Scores:


```

Pred. No.: 1,32e-169 Length: 1916
Score: 178.00 Matches: 278
Percent Similarity: 99.29% Conservative: 0
Best Local Similarity: 99.29% Mismatches: 1
Query Match: 34.43% Indels: 2
DB: 15 Gaps: 0

US-09-964-277-21 (1-517) x US-10-108-260A-2429 (1-1916)

Qy 239 AlaAspArgLeuGluAspSerLeuLysArgSerPheSerLeuAspIleLysSer 258
Db 142 GCAGACAGGCTGGAAGACAGCAATAGCTCAAGCGTTCCTCTCTCGATATCAATCA 201
Qy 259 ValSerTyrSerAlaSerMetAlaSerLeuHisGlyPheSerSerGluAspAla 278
Db 202 GTTTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCTCATCAGAGATGCT 261
Qy 279 LeuGluTyrTrpLysProSerThrThrLeuAspGlyThrAsnLysLeuCyseGlnPheSer 298
Db 262 TTGGAATACTACAAAGCTTCCACTACTCTGGATGGACCAACAGCTATGCCAGTTCTCC 321
Qy 299 ProValGlnGluSerGluGlnThrProGluThrSerProAspLysGluGluAlaSer 318
Db 322 CCTGTTCCAGAACTATCGGAGCAGATCCGAAACCGATCCCTGATAGAGGAGCCAGC 381
Qy 319 IleProLysLysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHisSer 338
Db 382 ATCCCAAGAAGCTGCAGACCGCCGCTTCAGACAGCCAGCAAGCGATTGCATTGC 441
Qy 339 ValArgThrSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisArgSer 358
Db 442 GTCCAGAACCCAGCAGCAGTGCACCGCCGAGAGTCCCTTTATCTCCACTGTCGAAGT 501
Qy 359 GlySerValGluAspAsnTyrHisThrSerPheLeuPheGlyLeuSerThr-SerGlnGln 378
Db 502 GGGAGCGTGGAGGACATATACACACAGCTCTTTCGGGCTTTCCAT-CAGCCAGCA 560
Qy 378 nHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaPr 398
Db 561 GCACCTCACGAAGTCTGCTGGCCCTTAAAGGCTGGCCTCGGATATCTTGGCCCC 620
Qy 398 oGlnThrSerThrProSerLeuThrSerSerTrpTyrPheAlaThrGluSerSerHisPh 418
Db 621 CCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTATTTTGGCCACAGAGTCTCACACT 680
Qy 418 eTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSerAlaTyrSerCyseSerG 438
Db 681 CTACTCTGCTCAGCCATCTACGAGGAGCAGTGCCTTACTCTGCTACAGCTGCAGCCA 740
Qy 438 nLeuProThrCysGlyAspGlnValTyrSerValArgArgArgGlnLysProSerAspAr 458
Db 741 GCTGCCACCTTGGGAGACCAAGTCTATCTGTGCGCAGCGGAGGAGGAGGAGGAG 800
Qy 458 gAlaAspSerArgArgSerTrpHisGluGluSerProPheGluLysGlnPheLysArgAr 478
Db 801 AGCTGACTCGCGCGGAGCTGCATGAAGAGAGCCCTTTGAAAGACAGTTTAAACGCGAG 860
Qy 478 gSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArgGluGluLe 498
Db 861 AAGCTGCAATGGAATTTTGGAGAGCAGCATCATGTGAGAGACAGGTACCGGGAAGAGCT 920
Qy 498 uGlyLysValGlySerGlnSerPheSerGlySerMetGluIleIleGluValSer 517
Db 921 GGGGAAGTGGCAGTCACTAGCTTTCGGGAGCAGCATGGAATCATTTAGGTCTCTCC 978

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RESULT 12

US-09-783-590-8120
; Sequence 8120, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong

```

; APPLICANT: Rosen, Craig A.  

; APPLICANT: Ruben, Steven M.  

; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  

; FILE REFERENCE: PO-16.2C1  

; CURRENT APPLICATION NUMBER: US/09/783,590  

; PRIOR FILING DATE: 2000-02-15  

; CURRENT APPLICATION NUMBER: 08/420,856  

; PRIOR FILING DATE: 1995-04-12  

; PRIOR APPLICATION NUMBER: 08/346,731  

; PRIOR FILING DATE: 1994-11-21  

; NUMBER OF SEQ ID NOS: 12485  

; SOFTWARE: PatentIn Ver. 2.0  

; SEQ ID NO 8120  

; LENGTH: 424  

; TYPE: DNA  

; ORGANISM: Homo sapiens  

; FEATURE:  

; NAME/KEY: misc feature  

; LOCATION: (10)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (65)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (128)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (167)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (199)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (237)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (246)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (250)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (255)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (272)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (277)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (290)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (291)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (292)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (298)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (300)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (317)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (328)  

; OTHER INFORMATION: n equals a,t,g, or c  

; NAME/KEY: misc feature  

; LOCATION: (331)

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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (335)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (365)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (395)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (403)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (404)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (413)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-8120

Alignment Scores:
Pred. No.: 6.7e-43 Length: 424
Score: 52.00 Matches: 52
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.06% Indels: 0
DB: 9 Gaps: 0

US-09-964-277-21 (1-517) x US-09-783-590-8120 (1-424)

QY 389 LysGlyTrpHisSerAspLeuAlaProGlnThrSerThrProSerLeuThrSerSer 408
DB 15 AAGGCTGGCATCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTNACCAGCAGC 74
QY 409 TrpTyrPheAlaThrGlnSerSerHisPheTyrSerAlaSerAlaLeuTyrGlySer 428
DB 75 TGGTATTTTGGCCACAGAGTCTTACACTTCTACTGCTCAGCCATCTAGGNGGCGAGT 134
QY 429 AlaSerTyrSerAlaTyrSerCysSerGlnLeuPro 440
DB 135 GCAGTTACTTCTGCTTACAGCTGCAGCCAGCTNCCC 170

RESULT 13
US-10-005-858-1
Sequence 1, Application US/10005858
Publication No. US20020116729A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NTTP1
FILE OF INVENTION: PHOSPHATASE GENE DISRUPTIONS
FILE REFERENCE: R-690
CURRENT APPLICATION NUMBER: US/10/005,858
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/251,802
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2453
TYPE: DNA
ORGANISM: Mus musculus
US-10-005-858-1

Alignment Scores:
Pred. No.: 6.96e-10 Length: 2453
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.87% Indels: 0
DB: 13 Gaps: 0

US-09-964-277-21 (1-517) x US-10-005-858-1 (1-2453)

QY 94 ValHisCysLeuAlaGlyTyrSerArgSerAlaThrIleAlaIleAlaTyrIleMetLys 113
DB 827 GTTCACCTGCTGGCTGGCATCTCTGCTGTGCCACCATTCGCCATCATCATGAAA 886
RESULT 14
US-09-964-824A-463/c
Sequence 463, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PatentIn version 3.0
SEQ ID NO 463
LENGTH: 263
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(263)
OTHER INFORMATION: n=a,t,g or c
US-09-964-824A-463

Alignment Scores:
Pred. No.: 0.0112 Length: 263
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.32% Indels: 0
DB: 9 Gaps: 0

US-09-964-277-21 (1-517) x US-09-964-824A-463 (1-263)

QY 92 ValLeuValHisCysLeuAlaGlyTyrSerArgSer 103
DB 105 GTCTTGTACATTCCTGCTGGCATTCAGCGNTCA 70

RESULT 15
US-09-880-107-1814/c
Sequence 1814, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1814
LENGTH: 263
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 F10276

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; NAME/KEY: unsure
; LOCATION: (1)..(263)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-1814

Alignment Scores:
Pred. No.:      0.0112      Length:      263
Score:          12.00       Matches:     12
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      2.32%      Indels:     0
DB:               9         Gaps:        0

US-09-964-277-21 (1-517) x US-09-880-107-1814 (1-263)

Qy      92 ValIeuValHisCysIeuAlaGlyIleSerArgSer 103
Db      105 GTCTTGGTACATTGCTTGGCTGGCATTAGCCGNICA 70

Search completed: February 28, 2004, 04:23:22
Job time : 532 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2004, 00:54:04 ; Search time 3854 Seconds
(without alignments)
4005.902 Million cell updates/sec

Title: US-09-964-277-21
Perfect score: 517
Sequence: 1 MFLSLQVFLSYFWNRR.....LGKVGSSFSFGSMIEIVS 517

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 1

Total number of hits satisfying chosen parameters: 55025477

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV-xml
-MODE=frame_p2n.model -DEV-xml
-Q=/cgn2_1/USPTO_spool/SUFFIX-olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -MAXLEN=200000000
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09964277@cgn.1.1.2810 -runat 25022004 085401 2218 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=30 -DELOP=6 -DELEXT=7

Database : EST.*
1: em estba.*
2: em esthum.*
3: em estin.*
4: em estmu.*
5: em estov.*
6: em estpl.*
7: em estro.*
8: em htc.*
9: gb est1.*
10: gb est2.*
11: gb htc.*
12: gb est3.*
13: gb est4.*
14: gb est5.*
15: em estfun.*
16: em estom.*
17: em gss hum.*
18: em gss inv.*
19: em gss pln.*
20: em gss vrt.*
21: em gss fun.*
22: em gss nam.*
23: em gss mus.*
24: em gss pro.*
25: em gss rod.*
26: em gss phg.*
27: em gss vrl.*
28: gb gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	216	41.8	903	12	BG482429	BG482429 602526595
2	209	40.4	891	13	BQ670889	BQ670889 AGENCOURT
3	186	36.0	1060	12	BM546940	BM546940 AGENCOURT
4	179	34.6	983	12	BG165188	BG165188 602344051
5	167	32.3	859	13	BQ933499	BQ933499 AGENCOURT
6	160	30.9	881	13	BQ930140	BQ930140 AGENCOURT
7	160	30.9	974	13	BQ951695	BQ951695 AGENCOURT
8	159	30.8	663	13	BX479029	BX479029 DKFP686J
9	139	26.9	883	13	BQ945892	BQ945892 AGENCOURT
10	130	25.1	391	13	EX475224	EX475224 DKFP686J
11	126	24.4	444	12	BM987142	BM987142 UI-H-COO-
12	126	24.4	920	10	BE897795	BE897795 601438457
13	124	24.0	621	9	AV703072	AV703072 AV703072
14	124	24.0	693	9	AV701628	AV701628 AV701628
15	101	19.5	660	12	BI917706	BI917706 603183686
16	96	18.6	463	10	BG058779	BG058779 raf10f04
17	96	18.6	682	12	BI816954	BI816954 imageqc_1
18	87	16.8	752	13	BQ432082	BQ432082 AGENCOURT
19	86	16.6	424	10	AW461438	AW461438 BP230005A
20	77	14.9	913	13	BU170187	BU170187 AGENCOURT
21	73	14.1	371	13	BX492954	BX492954 DKFP2781F
22	64	12.4	337	14	CB606296	CB606296 AMGNNUC-S
23	64	12.4	442	14	CB606149	CB606149 AMGNNUC-N
24	63	12.2	402	29	CG499793	CG499793 OST42180
25	63	12.2	404	10	BB816652	BB816652 BB816652
26	63	12.2	412	9	AA879894	AA879894 vW01G07.r
27	63	12.2	421	10	BE946884	BE946884 UI-M-BH3-
28	63	12.2	579	10	BF582366	BF582366 602094304
29	63	12.2	715	14	CF727177	CF727177 UI-M-HBO-
30	63	12.2	769	13	BU704078	BU704078 UI-M-FOO-
31	63	12.2	836	12	BI821804	BI821804 603035883
32	63	12.2	862	13	BQ770036	BQ770036 UI-M-F10-
33	63	12.2	946	12	BI657528	BI657528 603281866
34	61	11.8	386	10	BE983039	BE983039 UI-M-CGQD
35	61	11.8	476	28	AZ561697	AZ561697 RPCI-23-1
36	61	11.8	580	13	BQ568918	BQ568918 g118d07
37	61	11.8	634	14	CF733313	CF733313 UI-M-HBO-
38	61	11.8	680	13	BU613778	BU613778 UI-M-EMO-
39	61	11.8	723	13	BU708175	BU708175 UI-M-FCO-
40	61	11.8	1110	10	BF143207	BF143207 601787214
41	54	10.4	736	29	CE172184	CE172184 tigr-gss-
42	53	10.3	463	9	AA791519	AA791519 vs39g09.r
43	51	9.9	656	14	CF532917	CF532917 UI-M-GHO-
44	45	8.7	743	14	CF727802	CF727802 UI-M-HBO-
45	44	8.5	639	14	CF742387	CF742387 UI-M-HBO-

ALIGNMENTS

RESULT 1
BG482429
LOCUS 602526595F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4650430 5',
DEFINITION mRNA sequence.
ACCESSION BG482429
VERSION BG482429.1 GI:13414708
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 903)

AUTHORS

NH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLM1431 row: m column: 23

High quality sequence stop: 80%.

FEATURES

source

RESULT 2

BQ670989

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

ORIGIN

Alignment Scores:

Pred. No.: 1,96e-190 Length: 903

Score: 216.00 Matches: 216

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 41.78% Indels: 0

DB: 12 Gaps: 0

US-09-964-277-21 (1-517) x BG482429 (1-903)

Qy 30 GluLeuMetGlnGlnAnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
 Db 21 GAGTCGATGCGAGAGATGGATGGTTATGTTAAATCCAGCAATACCTGTCCAAAG 80
 Qy 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
 Db 81 CCGTACTTTATCCCGAGTCTCAATTCCTCGGTGCTGCTGGAATGACAGCTTTTGTGAG 140
 Qy 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGlyLeuAlaLysAlaSerAsn 89
 Db 141 AAAATTTTGGCGTGGTGGCAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCCAAT 200
 Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
 Db 201 GGATGTCTTAGTGCACTTTTAGTGGATCTCCCGTCCGCTCCGACCATGCTATCCGC 260
 Qy 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
 Db 261 TACATCATGAGAGAGTGGACATGCTTTAGATGAGCTTACAGATTGTGAAGAAAAA 320
 Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnLysLys 149
 Db 321 AGACCTACTATCTCCAAACTTTCAATTTTCTGGGCCAACTCTGAGCTATGAGAGAG 380
 Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
 Db 381 ATTAGAACCCAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTCTGACCTGGAG 440
 Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189

Db 441 AAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGGAGACGCCCTC 500
 Qy 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
 Db 501 AGTCCACCTGTGCGGACTCTGTACCTCAGAGCAGCAGCAAGAGCCCGTGCATCCC 560
 Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
 Db 561 GCACGGTGCACCGGCTGCCAGGCTGCCAGGCTGCCGCTGCTGTAGAGGACAGCCCTCGTA 620
 Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
 Db 621 CAGGCGCTCAGTGGCTGCACCTGTCCGACACAGAGGTGGAGACAGC 668

BQ670989 891 bp mRNA linear EST 15-JUL-2002
 AGENCOURT_8039377 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:6211589
 5', mRNA sequence.
 BQ670989
 BQ670989.1 GI:21781823
 EST.
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 891)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM2374 row: f column: 06
 High quality sequence stop: 63%.

FEATURES

source

1. .891

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6211589"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_102"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 6,48e-184 Length: 891

Score: 209.00 Matches: 209

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 40.43% Indels: 0

DB: 13 Gaps: 0

US-09-964-277-21 (1-517) x BQ670989 (1-891)

Qy 309 GluThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThrAlaArgPro 328
 Db 1 GAAACCAAGTCTCTGATAAGAGAGAACCCAGCATCCCCCAAGAGAGCTGCAGCCGCGCCT 60

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QY 329 SerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGln 348
Db 61 TCAGACAGCCAGCAAGCGATTGCTTCGGTCAAGACCAAGCAGCAGTGGCAGCCAG 120
QY 349 ArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAenTyrHisThrSer 368
Db 121 AGGTCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGACAATACCAACAGC 180
QY 369 PheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeu 388
Db 181 TTCCTTTTCGGCCTTTCCACAGCCAGCAGCAGCAGCTCAGGAAGTCTGCTGGCCTGGCCCTT 240
QY 389 LysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSer 408
Db 241 AAGGGCTGGCACTCGATATCTTGCCCCCAGACCTTACCCCTTCCCTGGACCAAGCAGC 300
QY 409 TrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlySer 428
Db 301 TGGTATTTTGGCACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGGAGCAGT 360
QY 429 AlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSer 448
Db 361 GCCAGTTACTCTGCTAGAGTGCAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCT 420
QY 449 ValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGlyGlu 468
Db 421 GTGCCAGGGCGCAGAACCCAGGTGACAGAGCTGCTCGCGCGAGCTGGCATGAGAG 480
QY 469 SerProPheGlyLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIle 488
Db 481 AGCCCTTTTGAAGACAGCTTTAAACCGCAGAGCTGCCAAATGGAAATTTGGAGAGAGCATC 540
QY 489 MetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSer 508
Db 541 ATGTCAAGAACAGCTCACGGAGAGAGTGGGAAAGTGGGCAGTCAGTCTAGCTTTTCG 600
QY 509 GlySerMetGluIleGluValSer 517
Db 601 GCAGCATGGAAATCATTTAGGTCTCC 627
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RESULT 3
BM546940
LOCUS
DEFINITION BM546940 1060 bp mRNA linear EST 20-FEB-2002
5', mRNA sequence.
AGENCOURT 6491295 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723711
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ACCESSION BM546940
VERSION BM546940.1 GI:18780310
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KEYWORDS EST.
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SOURCE Homo sapiens (human)
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```
ORGANISM Homo sapiens
```

```
REFERENCE 1 (bases 1 to 1060)
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```
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
```

```
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
```

```
JOURNAL Unpublished (1999)
```

```
COMMENT Contact: Robert Strausberg, Ph.D.
```

```
Email: cgabbs-remail.nih.gov
```

```
Tissue Procurement: Invitrogen
```

```
cDNA Library Preparation: Life Technologies, Inc.
```

```
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

```
DNA Sequencing by: Agencourt Bioscience Corporation
```

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Clone Distribution: MGC clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL at:
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http://image.llnl.gov
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Plate: LLAM12711 row: m column: 24
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High quality sequence stop: 737.
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Location/Qualifiers
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1..1060
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/organism="Homo sapiens"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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```
FEATURES
```

```
source
```

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/clone="IMAGE:5723711"
/lab host="DH10B"
/clone lib="NIH_MGC_125"
/notes="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
```

ORIGIN

```
Alignment Scores:
Pred. No.: 2,13e-162 Length: 1060
Score: 186.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.98% Indels: 0
DB: 12 Gaps: 0
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```
US-09-964-277-21 (1-517) x BM546940 (1-1060)
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QY 30 GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
Db 51 CAGCTGATGCAGCAGATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAG 110
QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 111 CCTGACTTATTCCTCCGAGTCTCATTTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 170
QY 70 LysIleLeuProTyrLeuAspLysSerValAspPheIleGlyLysAlaLysAlaSerAsn 89
Db 171 AAATTTTGGCTGGTGGCAATCATGATGATTTCTTGGAAAGCAAAAGCTCCCAT 230
QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 231 GGATGTGTTCTAGTGCACATGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC 290
QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 291 TACATCATGAGAGATGGACATGCTTTAGTAGTAAAGCTTACAGATTGTGAAAGAAATA 350
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 351 AGACCTACTATATCTCAAACTTCAATTTTCTGGCCAACTCTCTGGACTATGAGAAAGAG 410
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
Db 411 ATTAAGAACCAAGCTGGAGCATCAGGCGCCAAAGAGCAAACTCAAGCTGTGCACCTGGAG 470
QY 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
Db 471 AAGCAATGAACTGCTCCCTGCTGCTCTCAGAGGGTGGACAGAAAGCAGAGACGCCCTC 530
QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
Db 531 AGTCCACCTCTGTGCCGACTCTGTACCTACCTCAGAGCAGCAGGCAAAAGGCCCGCTGCC 590
QY 210 AlaSerValProSerVal 215
Db 591 GCCAGCTACCCAGCGTG 608
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RESULT 4

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BM546940
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LOCUS
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DEFINITION
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BM546940
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```
VERSION
```

```
BM546940.1
```

```
GI:12671891
```

```
KEYWORDS
```

```
EST.
```

```
Source
```

```
Homo sapiens (human)
```

```
BM546940 983 bp mRNA linear EST 06-FEB-2001
602344051F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4454029 5',
mRNA sequence.
```

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 983)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM10245 row: f column: 14
 High quality sequence stop: 625.
 Location/Qualifiers
 FEATURES
 source
 1. 983
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4454029"
 /tissue_type="hypernephroma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 89"
 /notes="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 6 6e-156 Length: 983
 Score: 179.00 Matches: 192
 Percent Similarity: 99.48% Conservative: 0
 Best Local Similarity: 99.48% Mismatches: 0
 Query Match: 34.62% Indels: 1
 DB: 12 Gaps: 0

US-09-964-277-21 (1-517) x BG165188 (1-983)

Qy 271 GlyPheSerSerGluAlaLeuGluTyrTyrPheSerThrThrLeuAspGly 290
 Db 2 GGCCTCTCTCATCAGAAGATGCTTTGGATACATCAAACTTCCACTACTCGATGG 61
 Qy 291 ThrAsnLysLeuGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThr 310
 Db 62 ACCAACAGCTATGCCAGTTCTCCCTGTTTCAGAACTATCGAGCAGACTCCGAAACC 121
 Qy 311 SerProAspLysGluAlaSerIleProLysLeuGlnThrAlaArgProSerAsp 330
 Db 122 AGTCCTGATAAGGAGGAGCCAGCATCCCAAGCTGCAGACTCCAGGCTTCAGAC 181
 Qy 331 SerGlnSerLysArgLeuHisSerValActThrSerSerGlyThrAlaGlnArgSer 350
 Db 182 AGCCAGAGCAGCGATTGCTATCGTTCAGAACCCAGCAGCAGTGGCACCCTCAGAGGCC 241
 Qy 351 LeuLeuSerProLeuHisArgSerGlySerValGluAspAsnThrHisThrPheLeu 370
 Db 242 CTTTTATCTCCATGTCATCGAAGTGGGAGCGTGGAGGACAAATACACACAGCTCCCTT 301
 Qy 371 PheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuLysGly 390
 Db 302 TTCGGCTTTCCACCCAGCAGCAGCCTCAGAACTGCTGGCTGGCTTAAAGGCG 361
 Qy 391 TrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpTyr 410
 Db 362 TGGCACTCGGATATCTTGGCCCCCCCCAGACTCTACCCCTTCCCTGACAGCAGCTGAT 421
 Qy 411 PheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSer 430

Db 422 TTTCGCACAGAGTCTCTACACTTCTACTCTGCTCAGCATCTACGGAGGAGTCCAGT 481
 Qy 431 TyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln-ValTyrSerValar 450
 Db 482 TACTCTGCTACAGCTGCGAGCAGTCCCTTTCGGAGACCAAGACTTATTCTGTGG 541
 Qy 450 GARGAGGlnLysProSerAspArgAlaAspSerArg 462
 Db 542 CAGCGCGCAGAGCCAGTGCAGAGCTGACTCGCGG 578

RESULT 5

BQ933499
 LOCUS BQ933499
 DEFINITION AGCOURT 8732489 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6455595
 5' mRNA sequence.

ACCESSION BQ933499

VERSION BQ933499.1 GI:22348882

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 859)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC2634 row: i column: 04

High quality sequence stop: 727.

Location/Qualifiers

FEATURES

source

1. 859

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6455595"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC_101"

/note="Organ: lung; Vector: pOTS7; Site 1: EcoRI; Site 2:

XhoI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G) Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 8 8e-145 Length: 859
 Score: 167.00 Matches: 267
 Percent Similarity: 99.26% Conservative: 0
 Best Local Similarity: 99.26% Mismatches: 1
 Query Match: 32.30% Indels: 2
 DB: 13 Gaps: 0

US-09-964-277-21 (1-517) x BQ933499 (1-859)

Qy 118 SerLeuAspGluAlaTyrArgPheValLysGluLysA-gProThrIleSerProAsn 137
 Db 3 TCTTAGATGAGCTTACAGATTGTGTAAGAAAAAGACCTACTATATCTCAAACTTC 62
 Qy 138 AsnPheLeuGlnLeuLeuAspTyrGluLysIleLysAsnGlnThrGlyAlaSer 157

Db 63 AATTTCCTGGCCAACTCTCGACTATGAGAGAGATTAAGAACACAGACTGGAGATCA 122
QY 158 GlyProLysSerLysLeuLysLeuHisLeuGluLysProAsnGluProValProAla 177
Db 123 GGGCCAAAGAGCAAACTCAAGCTGTGACCTGGAGAGCCAAATGAACCTGTCCCTGCT 182
QY 178 ValSerGluGlyGlyGlnLysSerGluThrProLeuSerProCysAlaAspSerAla 197
Db 183 GTCTCAGAGGGTGGACAGAAAGCCAGAGCCCTCAGTCCACCTGTGCCGACTCTGCT 242
QY 198 ThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerValProSerValProSer 217
Db 243 ACCTCAGAGGACAGGACAAAGGCCGTGATCCGCCAGCGTCCGCCAGC 302
QY 218 ValGlnProSerLeuLeuLysSerProLeuValGlnAlaLeuSerGlyLeuHisLeu 237
Db 303 GTGACAGCCCTGCTGTGAGAGACAGCCCGCTGTGACAGGGCCCTCAGTGGGCTCAGCTG 362
QY 238 SerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPheSerLeuAspIleLys 257
Db 363 TCCGACAGAGGCTGGAGACAGCAATAGCTCAAGCGTTCCTCTCTCTGGATATCAA 422
QY 258 SerValSerTySerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAsp 277
Db 423 TCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCTCTCTGATATCAA 482
QY 278 Ala-LeuGluTyTyTyTyProSerThrThrLeuAspGlyThrAsnLysLeuGlnPh 297
Db 483 GT-TTTGGAAATACAAACCTTCCACTACTCTGGATGGACCAACAGACTATGCCAGTT 541
QY 297 eSerProValGlnGluLeuSerGluGlnThrProGluThrSerProAspLysGluGluAl 317
Db 542 CTCCTCTGTTAGGAACCTATCGAGAGAGATTAAGAACACAGACTGGAGATCA 601
QY 317 aSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHi 337
Db 602 CAGCATCCCCAAGAGCTGCAGACCCGAGCGCTTTCAGACGCGAGCAAGCGATGGCA 661
QY 337 sSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisAr 357
Db 662 TTCGGTCAGAACACAGCAGCAGTGGACCGCCGACAGAGTCCCTTTATCTCCACTGCATCG 721
QY 357 gSerGlySerValGluAspAsnTyHisThrSerPheLeuPheGlyLeuSerThrSerGl 377
Db 722 AAGTGGAGCGTGGAGGACAATATACACACAGCTTCCTTTTCGGCCCTTTCCACAGCCA 781
QY 377 nGlnHisLeuThrLysSerAlaGly 385
Db 782 GCAGCACTCAAGAGTCTGCTGGC 806

RESULT 6
BQ930140
LOCUS
DEFINITION BQ930140 881 bp mRNA linear EST 20-AUG-2002
AGENCOURT 8923732 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6460964
5', mRNA sequence.
ACCESSION BQ930140
VERSION BQ930140.1 GI:22345171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2648 row: h column: 21
High quality sequence stop: 676.
Location/Qualifiers
1. 881
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6460964"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site: 1: EcoRI; Site: 2:
Xho; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 3.03e-138 Length: 881
Score: 160.00 Matches: 269
Percent Similarity: 98.90% Conservative: 0
Best Local Similarity: 98.90% Mismatches: 1
Query Match: 20.95% Indels: 3
DB: 13 Gaps: 0

US-09-964-277-21 (1-517) x BQ930140 (1-881)

QY 118 SerLeuAspGluAlaTyArgPheValLysGluLysArgProThrIleSerProAsnPhe 137
Db 3 TCTTTAGATGAGCTTACAGATTTGTGAAGAAAGACCTACTATATCTCCAACTTC 62
QY 138 AsnPheLeuGlyGlnLeuLeuAspTyGluLysLysIleLysAsnGlnThrGlyAlaSer 157
Db 63 AATTTCTGGGCCAACTCTCGACTATGAGAGAGATTAAGAACACAGACTGGAGATCA 122
QY 158 GlyProLysSerLysLeuLysLeuHisLeuGluLysProAsnGluProValProAla 177
Db 123 GGGCCAAAGAGCAAACTCAAGCTGTGACCTGGAGAGCCAAATGAACCTGTCCCTGCT 182
QY 178 ValSerGluGlyGlnLysSerGluThrProLeuSerProCysAlaAspSerAla 197
Db 183 GTCTCAGAGGGTGGACAGAAAGCGAGAGCGCCCTCAGTCCACCTGTGCCGACTCTGCT 242
QY 198 ThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerValProSerValProSer 217
Db 243 ACCTCAGAGGACAGGACAAAGGCCGTGATCCGCCAGCGTCCGCCAGC 302
QY 218 ValGlnProSerLeuLeuLysSerProLeuValGlnAlaLeuSerGlyLeuHisLeu 237
Db 303 GTGACAGCCCTGCTGTGAGAGACAGCCCGCTGTGACAGGGCCCTCAGTGGGCTCAGCTG 362
QY 238 SerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPheSerLeuAspIleLys 257
Db 363 TCCGACAGAGGCTGGAGACAGCAATAGCTCAAGCGTTCCTCTCTCTGATATCAA 422
QY 258 SerValSerTySerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAsp 277
Db 423 TCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCTCTCTGATATCAA 482
QY 278 Ala-LeuGluTyTyTyTyProSerThrThrLeuAspGlyThrAsnLysLeuGlnPh 297
Db 483 GT-TTTGGAAATACAAACCTTCCACTACTCTGGATGGACCAACAGACTATGCCAGTT 541
QY 297 eSerProValGlnGluLeuSerGluGlnThrProGluThrSerProAspLysGluGluAl 317
Db 542 CTCCTCTGTTAGGAACCTATCGAGAGAGATTAAGAACACAGACTGGAGATCA 601

QY 317 aSerIleProLysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHi 337
 Db 602 CAGCATCCCCAAGAGCTGCAGACCCGCCGCTTCAGACAGCCAGCAAGCGATTGCA 661
 QY 337 sSerValArgThrSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHiAr 357
 Db 662 TTCGTCAGAACCCAGCAGCAGTGGCAGCCGCCAGGATCCCTTTATCTCCACTGCATCG 721
 QY 357 gSerGlySerValGluAspAsnTyrHisThrSerPheLeu-PheGlyLeuSerThrSerG 377
 Db 722 AAGTGGGAGCGTGGAGGACAAATACCAACACAGCTTCCTTTTTCGGCCCTTCCACAGCC 781
 QY 377 InGlnHisLeuThrLysSerAlaGlyLeuGly 387
 Db 782 AGCAGCACTTCAGAGTCTGCTGCTGGG 813

RESULT 7
 BQ951695
 LOCUS
 DEFINITION AGNCOURT 8947130 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6461668
 5' mRNA sequence.

ACCESSION BQ951695
 VERSION BQ951695.1 GI:22367173

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 974)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

CONTACT Robert Strausberg, Ph.D.

EMAIL: ccgabs-remail.nih.gov

Tissue Procurement: ATCC

CNA Library Preparation: Rubin Laboratory

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Cloned Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LICM2650 row: f column: 05

High quality sequence stop: 617.

FEATURES

source

1..974

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6461668"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:

XhoI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3,36e-138 Length: 974

Score: 160.00 Matches: 241

Percent Similarity: 99.18% Conservative: 0

Best Local Similarity: 99.18% Mismatches: 1

Query Match: 30.95% Indels: 2

DB: 13 Gaps: 0

US-09-964-277-21 (1-517) x BQ951695 (1-974)

QY 118 SerLeuAspGluAlaTyrArgPheValLysGluLysArgProThrLeuSerProAsnPhe 137

Db 3 TCTTTAGATGAGCTTACAGATTTGTGAAGAAAAGACCTACTATATCTCCAACTTC 62
 QY 138 AsnPheLeuGlyGlnLeuLeuAspTyrGlnLysLysIleLysAsnGlnThrGlyAlaSer 157
 Db 63 AATTTTCTGGCCAACTCTCTGACTATGAGAAGAAGATTAAAGAACCAGACTGGAGCATCA 122
 QY 158 GlyProLysSerLysLeuLysLeuLeuHisLeuGluLysProAsnGluProValProAla 177
 Db 123 GGGCCAAAGAGCAAACTCAGCTGCTGCACCTGGAGAACCAATGAACCTGTCCTGCT 182
 QY 178 ValSerGluGlyGlyGlnLysSerGlnThrProLeuSerProProCysAlaAspSerAla 197
 Db 183 GTCTCAGAGGGTGGACAGAAAAGCAGACGCCCTCAGTCCACCCCTGTCGCCACTGCT 242
 QY 198 ThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerValProSerValProSer 217
 Db 243 ACCTCAGAGCGCAGCAGCAAAAGGCCCTGTCATCCGCCAGCGTCCCGAGGTGCCAGC 302
 QY 218 ValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeu 237
 Db 303 GTGCAGCGCTCGCTGTTAGAGGACAGCCCGCTGGTACAGGGCGCTCAGTGGGCTGCACCTG 362
 QY 238 SerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPheSerLeuAspIleLys 257
 Db 363 TCCGCAGACAGCGTGGAGACAGCAATAAGCTCAAGCGTCTCTCTCTGATATCAAA 422
 QY 258 SerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAsp 277
 Db 423 TCAGTTTCATATTCAGCAGCATGCGCAGCATCTTTACATGGCTTCTCTCATCAGAAGAT 482
 QY 278 Ala-LeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPh 297
 Db 483 GT-TTTTGAATACTACAAACCTTCCACTACTCTGGATGGACCAACAGCTATGCCAGTT 541
 QY 297 eSerProValGlnGluLeuSerGluGlnThrProGluThrSerProAspLysGluGluAl 317
 Db 542 CTCCTCTGTTTCAGAACTATCGAGCAGACTCCCGAACCACTCTCTGATAGGAGGAGC 601
 QY 317 aSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHi 337
 Db 602 CAGCATCCCCAAGAGCTGCAGACCGCCAGGCTTCAGACAGCCAGCAAGCGATTGCA 661
 QY 337 sSerValArgThrSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHiAr 357
 Db 662 TTCGGTCAGAACCCAGCAGCAGTGGCAGCCGCCAGGCTTCAGACAGCCAGCAAGCGATTGCA 721
 QY 357 gSerGly 359
 Db 722 AAGTGGG 728

RESULT 8

BX479029

LOCUS

DEFINITION

DXFZ5686J22208 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

DXFZ5686J22208 5', mRNA sequence.

ACCESSION BX479029

VERSION BX479029.1 GI:31914415

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 663)

REFERENCE

AUTHORS

Behr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Osanger, A.,

Robo, G., Han, M., and Wiemann, S.

EST (Behr, A., Lauber, J., Mewes, H.W., Weill, B., et al.)

Unpublished (2003)

CONTACT: MIPS

COMMENT

MIPS

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.

No s1 sequence available.
This clone (DKFZp686J22208) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
1..663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686J22208"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Alignment Scores:
Pred. No.: 1,93e-137 Length: 663
Score: 159.00 Matches: 190
Percent Similarity: 98.96% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 1
Query Match: 30.75% Indels: 2
DB: 13 Gaps: 0

US-09-964-277-21 (1-517) x BX479029 (1-663)

QY 92 ValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaLeIaIaTyrIle 111
DB 57 GTTCTAGTGCACCTTTAGCTGGGATCTCCGGTCCGCCACCATCGCTATCGCTACATC 116
QY 112 MetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgPro 131
DB 117 ATGAGAGGATGGACATGCTTTAGATGAAGCTTACAGATTGTGAAGAAAAAGACCT 176
QY 132 ThrIleSerProAanPheAanPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLys 151
DB 177 ACTATATCTCCAAACTTCAATTTCTCGGCCAACTCTCGGACTATGAGAAGAATTAG 236
QY 152 AsnGlnThrGlyAlaSerGlyProLysSerLysLysLeuLysLeuHisLeuGluLysPro 171
DB 237 AACCAAGCTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGCCA 296
QY 172 AsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerPro 191
DB 237 AATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGCGCCCTCAGTCCA 356
QY 192 ProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSer 211
DB 357 CCCTGTGCCGACTCTGTCTACCTCAGAGCGACAGGACAAAGGCCGCTGCATCCCGCAGC 416
QY 212 ValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 231
DB 417 GTGCCACGCGCCAGCGTGCAGCCGCTGCTGTGTAGAGGACAGCCGCTGGTACAGGCG 476
QY 232 LeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLysLysArgSer 251
DB 477 CTCAGTGGGCTGCACCTCTCCGACAGACAGGCTGGAGACAGCAATAGCTCAAGCGTNC- 535
QY 252 -PheSerLeuAspLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGln 271
DB 536 CTTCTCTGTGATATCAAAATCAGTTTCATATTCAGCCAGCATGCGCATCTCTTACATGG 595
QY 271 yPheSerSerGluAspAlaLeuGluTyrTyr 282
DB 596 CTTCTCTCTCATCAGAGATGCTTTGGATACTAC 629

RESULT 9
BQ945892
LOCUS BQ945892 883 bp mRNA linear EST 21-AUG-2002

DEFINITION AGENCOURT_8926314 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6463045
5', mRNA sequence.

ACCESSION BQ945892

VERSION BQ945892.1 GI:22361370

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-f@mail.nih.gov

Tissue Procurement: AFCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM2653 row: 0 column: 14

High quality sequence stop: 672.

FEATURES

source

1..883

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6463045"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 101"

/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:

XhoI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACCAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1,14e-118 Length: 883

Score: 139.00 Matches: 249

Percent Similarity: 98.42% Conservative: 0

Best Local Similarity: 98.42% Mismatches: 2

Query Match: 26.89% Indels: 4

DB: 13 Gaps: 0

US-09-964-277-21 (1-517) x BQ945892 (1-883)

QY 139 PheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLysAsnGlnThrGlyAlaSerGly 158

DB 63 TTTCTGGGCCAACTCTCTGGACTATGAGAAGAGATTAGAACACAGCTGGACATCAGGG 122

QY 159 ProLysSerLysLysLeuLeuHisLeuGluLysProAsnGluProValProAlaVal 178

DB 123 CCAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGCCAAATGAACCTGCTCCCTGCTGTC 182

QY 179 SerGluGlyGlnLysSerGluThrProLeuSerProCysAlaAspSerAlaThr 198

DB 183 TCAGAGGGTGGACAGAAAAGCGAGAGCGCCCTCAGTCCACCTGTGCCACTCTGTCTACC 242

QY 199 SerGluAlaAlaGlyGlnArgProValHisProAlaSerValProSerValProSerVal 218

DB 243 TCAGAGGACAGCAGCAAAAGGCCGCTGCATCCGCCAGCGTGCACCGCTGCCAGCGTG 302

QY 219 GlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSer 238

DB 303 CAGCCGCTGCTGTAGAGGACAGCCCGCTGGTACAGCGCTCAGTGGGCTGACCTGCTGCC 362

Qy 239 AlaAspArgLeuGluAspSerLeuLysLeuLysArgSerPheSerLeuAspIleLysSer 258
 Db 363 GCAGACAGGCTGGAACACAGCAATAGCTCAAGCGTTCCTCTCTCTGGATCAAAATCA 422
 Qy 259 ValSerTySerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerGluAspAla 278
 Db 423 GTTTCATATTCACCCAGCATGGCAGCATCTTACATGGCTTCTCTCATCAGAGATGT- 481
 Qy 279 -LeuGluTyTyTyLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSe 298
 Db 482 TTTTGGAAATACTACAAACCTTCCACTACTCTGGATGGACCAACAGCTATGCCAGTTCTC 541
 Qy 298 rProValGlnGluLeuSerGluGlnThrProGluThrSerProAspLysGluGluAlaSe 318
 Db 542 CCTGTTCAGAACTATCGGAGCAGACTCCCGAAACCACTCTGATAGGAGGAGGACGAG 601
 Qy 318 rIleProLysLysLeuGlnThrAlaArgProSerAspSerGlnSerLysArgLeuHisSe 338
 Db 602 CATCCCCAAGAAGCTGCAGACCCGACAGGCTTCAGACAGCCAGAGCAAGCGATTGCATTC 661
 Qy 338 rValArgThr-SerSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisArgS 358
 Db 662 GGTGAGAAA-CAGCAGCAGTGGCAGCCGCGCCAGAGTCCCTTTATCTCCACTGGATCGAA 720
 Qy 358 erGlySerValGluAspAsnTyHisThrSerPheLeuPheGlyLeuSerThrSerGlnG 378
 Db 721 GTGGAGCGTGGAGCAATATACACACAGCTTCCTTTTCGGCTTTCACACGCCAGC 780
 Qy 378 InHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
 Db 781 AGCACCTCAGCAAGTCTGTGGCTGGCTGGGCTTAAG 815
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 LOCUS DXFZp686J02209_r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
 DEFINITION DXFZp686J02209 5', mRNA sequence.
 ACCESSION EX479224
 VERSION EX479224.1 GI:31914811
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 391)
 AUTHORS Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
 Fobo, G., Han, M. and Wiemann, S.
 TITLE EST (Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., et al.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No s1 sequence available.
 This clone (DXFZp686J02209) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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 Qy 114 ArgMetAspMetSerLeuAspGluAlaTyArgPheValLysGluLysArgProThrIle 133
 Db 62 AGGATGGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAGAACCTACTATA 121
 Qy 134 SerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyGlyLysLysIleLysAsnGln 153
 Db 122 TCTCCAACTTCAATTTCTGGGCCCACTCTCTGACTATGAGAAAGAGATTAGAACAG 181
 Qy 154 ThrGlyValAspSerGlyProLysSerLysLeuLysLeuHisLeuGluLysProAsnGlu 173
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 Qy 174 ProValProAlaValSerGlyGlyGlnLysSerGluThrProLeuSerProProCys 193
 Db 242 CCTGCTCCCTGCTGTCAGAGGGTGGACAGAAAAGCGAGCGCCCTCAGCCACCTGT 301
 Qy 194 AlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerValPro 213
 Db 302 GCGCACTGCTGCTACTCTCAGAGCAGCAGCAGCAGAGCCGCTGCATCCGCCAGCGTGC 361
 Qy 214 SerValProSerValGlnProSerLeuLeu 223
 Db 362 AGCGTCCCGAGCGTGCAGCGCTGCTGTTA 391
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 444)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapb@remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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 POLYA=Yes.
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VERSION AV703072.1 GI:10719402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,
Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,
Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,
Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
TITLE Chinese National Human Genome Center at Shanghai
JOURNAL 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
COMMENT 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 23.98% Indels: 0
DB: 9 Gaps: 0
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QY 222 LeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArg 241
Db 198 CTGTTAGAGACAGCCCGTGTGTACAGGCGCTCAGTGGCTGCACCTGTCCGCGACAGG 257
QY 242 LeuGluAspSerAsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyr 261
Db 258 CTGGAAGACAGCAATAAGCTCAAGCGTCTCTCTCTCTGATATCAATCAGTTTCATAT 317
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Db 318 TCAGCCAGCATGGCAGCATCTTACATGCTTCTCTCTCTGATATCAATCAGTTTCATAT 377
QY 282 TyrLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGln 301
Db 378 TACAACCTTCCACTACTCTGGATGGGACCAACAGCTATGCCAGTCTCCCTGTTTCAG 437
QY 302 GluLeuSerGluGlnThrProGluThrSerProAspLysGluGluAlaSerIleProLys 321
Db 438 GAATCTCGAGGAGAGATCCCGAAACAGTCTCTGATAGGAGAGAGCCAGCATCCCCAAG 497

QY 322 LysLeuGlnThr 325
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ACCESSION AV701628
VERSION AV701628.1 GI:10717958
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 693)
AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,
Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,
Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,
Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
TITLE Chinese National Human Genome Center at Shanghai
JOURNAL 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
COMMENT 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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XhoI"
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Alignment Scores:
Pred. No.: 8,5e-105 Length: 693
Score: 124.00 Matches: 124
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 23.98% Indels: 0
DB: 9 Gaps: 0
US-09-964-277-21 (1-517) x AV701628 (1-693)
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QY 222 LeuLeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArg 241
Db 198 CTGTTAGAGACAGCCCGCTGCATCCGCGAGCGTGCAGCGTGCAGCGTGCAGCGCTCG 257
QY 242 LeuGluAspSerAsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyr 261
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Db 318 TCAGCCAGCATGGCAGCATCTTACATGCTTCTCTCTCTGATATCAATCAGTTTCATAT 377
QY 282 TyrLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGln 301
Db 378 TACAACCTTCCACTACTCTGGATGGGACCAACAGCTATGCCAGTCTCCCTGTTTCAG 437

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2004, 18:39:38 ; Search time 12757 Seconds
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Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: gb.pat.*
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9: gb.pr.*
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40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3332	100.0	3332	6	AX441229	AX441229 Sequence
2	3158	94.8	3496	6	AX441210	AX441210 Sequence
3	3145	94.4	3566	9	AF506796	AF506796 Homo sapi
4	3133.4	94.0	3521	9	AB052156	AB052156 Homo sapi
5	3118.8	93.6	3766	6	AX374994	AX374994 Sequence
6	3106.2	93.2	5450	6	AX482439	AX482439 Sequence
7	3106.2	93.2	5450	6	AX482478	AX482478 Sequence
8	2950	88.5	3544	6	AX260340	AX260340 Sequence
9	2924.6	87.8	5111	6	AX482372	AX482372 Sequence
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13	2766.4	83.0	4790	6	AB051487	AB051487 Homo sapi
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15	2710	81.3	3059	6	AX278461	AX278461 Sequence
16	2437.4	73.2	2807	9	BC031643	BC031643 Homo sapi
17	2390.8	71.8	2732	6	AX180875	AX180875 Sequence
18	2111.4	63.4	172206	9	AC007619	AC007619 Homo sapi
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21	1935	58.1	1935	9	AY038927	AY038927 Homo sapi
22	1822.6	54.7	4943	10	BC059232	BC059232 Mus muscu
23	1822.6	54.7	4975	10	BC057321	BC057321 Mus muscu
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27	1774	53.2	4982	10	AF345951	AF345951 Mus muscu
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29	1762.4	52.9	2102	9	AK055973	AK055973 Homo sapi
30	1742	52.3	2200	6	AX921915	AX921915 Sequence
31	1741	52.3	2118	6	AX099933	AX099933 Sequence
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33	1660	49.8	1998	6	AX260342	AX260342 Sequence
34	1638.2	49.2	2756	6	AX482444	AX482444 Sequence
35	1133	34.0	201474	2	AC126692	AC126692 Mus muscu
36	1133	34.0	236589	2	AC118035	AC118035 Mus muscu
37	1133	34.0	250782	2	AC128093	AC128093 Rattus no
38	964.2	28.9	242590	2	AC133722	AC133722 Rattus no
39	962.4	28.9	244605	2	AC097818	AC097818 Rattus no
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ALIGNMENTS

RESULT 1	AX441229	AX441229	3332 bp	DNA	linear	PAT 28-JUN-2002
LOCUS	AX441229	Sequence 20 from Patent WO0226597.				
DEFINITION	AX441229					
ACCESSION	AX441229					
VERSION	AX441229.1	GI:21665771				
KEYWORDS						
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ORGANISM	Homo sapiens (human)					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE						
AUTHORS	Luche, R.M. and Wei, B.					
TITLE	Dsp-16 dual-specificity phosphatase					
JOURNAL	Patent: WO 0226597-A 20 04-APR-2002;					

1981	DB	CACGAAGTCTGCTGGCCCTGGGCGCTTAAAGGCGCTGGCACTCGGAATCTTTGGCGCCCCCAGAC	2040
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2101	DB	TGCTCTCAGCATCTACGGAGGCAAGTCCAGTTACTCTGCCTACAGCTCAGCTGACGACGCTGCC	2160
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Qy	3121	CCCGTGGCGCTAGATGGAGATAAATTTTTTTTTTCTCTCAGCTTTATGTAAGAGACGAGAA	3180
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Db	3181	CTGCTTAGGATTCAGCTGAACCCACGAGAACCTGGCAACATCACGATTTAAAGCTTAAGGTT	3240
Qy	3241	GGGAGGCTAAAGAGTCTACCTCCCTCTTGTAAATCAAGAAATGTTTTAAATGGGATTG	3300
Db	3241	GGGAGGCTAAAGAGTCTACCTCCCTCTTGTAAATCAAGAAATGTTTTAAATGGGATTG	3300
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RESULT 2			
AX441210			
LOCUS	AX441210	3496 bp	DNA
DEFINITION	Sequence 1 from Patent WO0226997.		
ACCESSION	AX441210		
VERSION	AX441210.1	GI:21665766	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	LucHE, R.M. and Wei, B.	
AUTHORS		Dep-16 dual-specificity phosphatase	
TITLE		Patent: WO 0226997-A 1 04-APR-2002;	
JOURNAL		Cepryr, Inc. (US)	
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ORIGIN			
Query Match	94.8%;	Score 3158;	DB 6; Length 3496;
Best Local Similarity	95.3%;	Pred. No. 0;	
Matches 3332;	Conservative 0;	Mismatches 0;	Indels 164; Gaps 1;
Qy	1	GAGAGAGGAGAGATATATCTCTGAAAGAGAGGAGGAGAGCGACCGGAC	60
Db	1	GAGAGAGGAGAGATATATCTCTGAAAGAGAGGAGGAGAGCGACCGGAC	60
Qy	61	GGGAGGGGAGCGAGCGCCCTCTCGCTCCGCGGCGGCGCTCGAAGTCCGGGAGGC	120
Db	61	GGGAGGGGAGCGAGCGCCCTCTCGCTCCGCGGCGGCGCTCGAAGTCCGGGAGGC	120
Qy	121	GAGGGGGGCGCGGAGGAGCGCGTGCACAACTTTTCCTCTGAGGGAATGGGAG	180
Db	121	GAGGGGGGCGCGGAGGAGCGCGTGCACAACTTTTCCTCTGAGGGAATGGGAG	180
Qy	181	GTGCGGGGCGCCAAAGCTTTCAGTCCAGTGAAGAGCTGTCGAGCGCGGAGCAAGGT	240
Db	181	GTGCGGGGCGCCAAAGCTTTCAGTCCAGTGAAGAGCTGTCGAGCGCGGAGCAAGGT	240
Qy	241	AAAGAAATGATGTAAATGGCGTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATTC	300
Db	241	AAAGAAATGATGTAAATGGCGTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATTC	300
Qy	301	AGTCATCTTTTATGATCAAAATGTAGGGGCTCTTCTGTCGACGAGTCCCTTTCGAAGA	360
Db	301	AGTCATCTTTTATGATCAAAATGTAGGGGCTCTTCTGTCGACGAGTCCCTTTCGAAGA	360
Qy	361	GCACATCAACGGGAAAGAGACATTCCTTCGAGGGCTCTTCTGCGAAATGGGTT	420
Db	361	GCACATCAACGGGAAAGAGACATTCCTTCGAGGGCTCTTCTGCGAAATGGGTT	420

421 TAACTCTCTCTTTGGCAGTGCACACAGCCTGACCTCATACACTTTTGTAGTACAAATGGAGT 480 QY
421 TAACTCTCTCTTTGGCAGTGCACACAGCCTGACCTCATACACTTTTGTAGTACAAATGGAGT 480 Db
481 GGCTGAGCCTTTGAGCACACACACCAATTAACATCATCTGTCGCAAAATTAAGAGAGAGTGGG 540 QY
481 GGCTGAGCCTTTGAGCACACACACCAATTAACATCATCTGTCGCAAAATTAAGAGAGAGTGGG 540 Db
541 AAAAGAGGACTTATTTGTTGTCATGTCGCAAAATTAAGAGAGAGTGGG 600 QY
541 AAAAGAGGACTTATTTGTTGTCATGTCGCAAAATTAAGAGAGAGTGGG 600 Db
601 AGTTGTTGGCTCTCTGTCGCAAAATTAAGAGAGAGTGGG 660 QY
601 AGTTGTTGGCTCTCTGTCGCAAAATTAAGAGAGAGTGGG 660 Db
661 TTTGTGGAATAAATATACATATTTGGAAGCCTTAAATATCAACTCAAGCTT 720 QY
661 TTTGTGGAATAAATATACATATTTGGAAGCCTTAAATATCAACTCAAGCTT 720 Db
721 ATGAGAGGAGCTTGAACAGGAGAGTGAATTAATACAGAGCTCATCCAGCATTCAAGG 780 QY
721 ATGAGAGGAGCTTGAACAGGAGAGTGAATTAATACAGAGCTCATCCAGCATTCAAGG 780 Db
781 AAACATAGAGTTGACATTTGGAAGCCTTAAATATCAACTCAAGCTTCAAGCTT 840 QY
781 AAACATAGAGTTGACATTTGGAAGCCTTAAATATCAACTCAAGCTTCAAGCTT 840 Db
841 GATGTTGCTCTCTCTGTCGCAAAATTAAGAGAGAGTGGG 900 QY
841 GATGTTGCTCTCTCTGTCGCAAAATTAAGAGAGAGTGGG 900 Db
901 AGCTTCAACTCTGTTCACTGCTTGC - 926 QY
901 AGCTTCAACTCTGTTCACTGCTTGC - 926 Db
927 - 927 QY
961 GGCCCTCTGTGAAGGAAATFCACTAGTCCCTACCTGCAATTTCTCAGCCTTGTCTTACCT 1020 Db
927 - 927 QY
1021 GTTGCCAACTATGGGCAACCCGAAATCTTCCCAATCTTTATCTTGGCTGCGCAGGAGAT 1080 Db
927 - 927 QY
1081 GTCCCTCAACAAAGAGCTGATGAGAGAGTGGGATTTGTTATGTTTAAATGCCAGCAAT 1140 Db
977 ACCTGTCGCAAGCCTGACCTTTATCCCGAGTCTCATTTCTGCGTGCCTGTGTAATGAC 1036 QY
1141 ACCTGTCGCAAGCCTGACCTTTATCCCGAGTCTCATTTCTGCGTGCCTGTGTAATGAC 1200 Db
1037 AGCTTTTGTGAGAAATTTTGGCGTGGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCA 1096 QY
1201 AGCTTTTGTGAGAAATTTTGGCGTGGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCA 1260 Db
1097 AAGCCCTCAGATGATGTTCTAGTGCATCTTTAGTGGATCTCCCGTCCGCGCACC 1156 QY
1261 AAGCCCTCAGATGATGTTCTAGTGCATCTTTAGTGGATCTCCCGTCCGCGCACC 1320 Db
1157 ATGCTATCCCTTACATGAGAGAGTGGACATGTTCTTTAGATGAAGCTTTTACAGATTT 1216 QY
1321 ATGCTATCCCTTACATGAGAGAGTGGACATGTTCTTTAGATGAAGCTTTTACAGATTT 1380 Db
1217 GTGAAGAAAGAAAGACTTATATCTCCAACTTCAATTTTCTGGGCAACTCTGAGAC 1276 QY
1381 GTGAAGAAAGAAAGACTTATATCTCCAACTTCAATTTTCTGGGCAACTCTGAGAC 1440 Db
1277 TATGAGAGAGAGATTAAGAACACAGCTGAGATCAGGCGCCAAAGAGCAAACTCAAGCTG 1336 QY
1441 TATGAGAGAGAGATTAAGAACACAGCTGAGATCAGGCGCCAAAGAGCAAACTCAAGCTG 1500 Db
1337 CTGCACCTGAGAGAGCAAAATGAACCTGTCCTGCTGCTCTCAGAGGTTGGACAGAAAGC 1396 QY

1501 CTGCACTGGAGAGCCAAATGAACCTGTCCCTGTCTCTCAGAGGTTGGACAGAAAGC 1560 Db
1397 GAGAGCCCTTCACTGTCACCTGTGCGGACTCTGCTACCTCAGAGCAGCAGCAGCAAGG 1456 QY
1561 GAGAGCCCTTCACTGTCACCTGTGCGGACTCTGCTACCTCAGAGCAGCAGCAGCAAGG 1620 Db
1457 CCGTGTATCCGCGCAGCTGCGCAGCCTGCCAGCGGTGAGCGCTGCTGTTAGAGGAC 1516 QY
1621 CCGTGTATCCGCGCAGCTGCGCAGCCTGCCAGCGGTGAGCGCTGCTGTTAGAGGAC 1680 Db
1517 AGCCCGCTGTGTAAGGCGCTCAGTGGGCTGACCTGTCGCGCAGCAGGCTGGAGACAGC 1576 QY
1681 AGCCCGCTGTGTAAGGCGCTCAGTGGGCTGACCTGTCGCGCAGCAGGCTGGAGACAGC 1740 Db
1577 AATAAGCTCAAGCGTTCTCTCTCTGATATCAAAATCAATCACTTATATTCAGCAGCAGT 1636 QY
1741 AATAAGCTCAAGCGTTCTCTCTCTGATATCAAAATCAATCACTTATATTCAGCAGCAGT 1800 Db
1637 GCAGCATCTTACATGCTTCTCTCATCAGAGAGTCTTTGGAATCACTACAAACCTTCC 1696 QY
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1697 ACTACTCTGATGGAGCAACAGCTATGCGCTCTCCCTGTTCAGGAACCTATCGAG 1756 QY
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1757 CAGATCTCCGAAACAGCTCTGTATGAGAGAGAGCAGCATCCCAAGAGCTGCGAGC 1816 QY
1921 CAGATCTCCGAAACAGCTCTGTATGAGAGAGAGCAGCATCCCAAGAGCTGCGAGC 1980 Db
1817 GCAGGCTTTCAGAGCAGCAGAGAGAGTTCGCTCAGAGCAGCAGCAGCAGCAGTGGC 1876 QY
1981 GCAGGCTTTCAGAGCAGCAGAGAGAGTTCGCTCAGAGCAGCAGCAGCAGCAGTGGC 2040 Db
1877 ACAGGCTCAGAGCTTCTTTTATCTCCACTGATCGAAGTGGAGCGTGGAGCAATTC 1936 QY
2041 ACAGGCTCAGAGCTTCTTTTATCTCCACTGATCGAAGTGGAGCGTGGAGCAATTC 2100 Db
1937 CACACAGCTTCTTTTTCGCTTTCAGAGCAGCAGCAGCAGCAGCAGCAGTGGC 1996 QY
2101 CACACAGCTTCTTTTTCGCTTTCAGAGCAGCAGCAGCAGCAGCAGTGGC 2160 Db
1997 CTGGGCTTTCAGAGCTTCTGCTGCTGAGCAGCAGCAGCAGCAGCAGTGGC 2056 QY
2161 CTGGGCTTTCAGAGCTTCTGCTGCTGAGCAGCAGCAGCAGCAGCAGTGGC 2220 Db
2057 ACCAGCAGCTGATTTTTCGCTTTCAGAGCTTCTCAGCTTCTGCTCAGCAGCAGTGGC 2116 QY
2221 ACCAGCAGCTGATTTTTCGCTTTCAGAGCTTCTCAGCTTCTGCTCAGCAGCAGTGGC 2280 Db
2117 GGAGGCTTTCAGAGCTTCTGCTGCTGAGCAGCAGCAGCAGCAGCAGTGGC 2176 QY
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2177 GTCTATTCTGTCGAGCAGCAGCAGCAGCAGCAGCAGCAGTGGC 2236 QY
2341 GTCTATTCTGTCGAGCAGCAGCAGCAGCAGCAGCAGCAGTGGC 2400 Db
2237 CATGAAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTGGC 2296 QY
2401 CATGAAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTGGC 2460 Db
2297 GAGAGCATCATGTCAGAGCAACAGCTTTCAGAGCAGCAGCAGCAGCAGTGGC 2356 QY
2461 GAGAGCATCATGTCAGAGCAACAGCTTTCAGAGCAGCAGCAGCAGTGGC 2520 Db
2357 AGCTTTTTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTGGC 2416 QY
2521 AGCTTTTTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTGGC 2580 Db
2417 CTATAGACAAATTTTTCGCTTTCAGAGCAGCAGCAGCAGCAGCAGTGGC 2476 QY

Dd		243	AAGAATGANTGTAACTGGCTGCCCTCAAAGCATCTTTTGTGTGGAAATGGTTATTCC	302
Qy		301	AGTCATCTCTTTTATGAATAAATGTGAGGGCGTGCTTTGTGGACGGAGTCCTTTTGCAGA	360
Dd		303	AGTCATCTCTTTTATGAATAAATGTGAGGGCGTGCTTTGTGGACGGAGTCCTTTTGCAGA	362
Qy		361	GCAATCTAACGGGAAGAAAGACAATTCACTTGGAGGGCTCTTGTGAAAATGGGTT	420
Dd		363	GCAATCTAACGGGAAGAAAGACAATTCACTTGGAGGGCTCTTGTGAAAATGGGTT	422
Qy		421	TAACTCTCTTTTTTGGCAGTACCACCGCTGACCTCATACACTTTTTAGTACAATGGAGT	480
Dd		423	THACTCTCTTTTGGCAGTACCACCGCTGACCTCATACACTTTTTAGTACAATGGAGT	482
Qy		481	GGCTGAGGCTTTGAGCACACCACTATCATCTGTTGGCAAAATTAAGAAGAGAGGTGGG	540
Dd		483	GGCTGAGGCTTTGAGCACACCACTATCATCTGTTGGCAAAATTAAGAAGAGAGGTGGG	542
Qy		541	AAAAAGAGCAATTATTTGTTCATCGCCCATTAGATGATTTGGAACCAAAATTGTTACTGAG	600
Dd		543	AAAAAGAGCAATTATTTGTTCATCGCCCCATTAGATGATTTGGAACCAAAATTGTTACTGAG	602
Qy		601	AGGTTGGTGGCTTGTCTGGAAGTGGAAACGGAAAAAGTGTCTTAATTGATAGCCGGCCA	660
Dd		603	AGGTTGGTGGCTTGTCTGGAAGTGGAAACGGAAAAAGTGTCTTAATTGATAGCCGGCCA	662
Qy		661	TTTGTGGBAATCAATACATCCCACTTTTGGAGGCCATTAATCAACTGTCTCCAGGCTT	720
Dd		663	TTTGTGGBAATCAATACATCCCACTTTTGGAGGCCATTAATCAACTGTCTCCAGGCTT	722
Qy		721	ATGAAGCGAAGGTTGCAACAGGCAAAAAGTGTAAATTACAGAGCTCATCCAGCAITTCAGCG	780
Dd		723	ATGAAGCGAAGGTTGCAACAGGCAAAAAGTGTAAATTACAGAGCTCATCCAGCAITTCAGCG	782
Qy		781	AAACATAGGTTGACATTTGATTCGAGTCAGAGGTTGTAGTTTAGATCAAAAGCTCCCA	840
Dd		783	AAACATAGGTTGACATTTGATTCGAGTCAGAGGTTGTAGTTTAGATCAAAAGCTCCCA	842
Qy		841	GATGTGGCTCTCTCTTTCAGACTGTTTTCTCACTGTACTCTGGGTAACCTGGAGAAG	900
Dd		843	GATGTGGCTCTCTCTTTCAGACTGTTTTCTCACTGTACTCTGGGTAACCTGGAGAAG	902
Qy		901	AGCTTCAACTCHGTTCACTGGCTTGC-----	926
Dd		903	AGCTTCAACTCHGTTCACTGGCTTGCAGSGTGGGTTTGTCTCTGGTGTGTTTCCCT	962
Qy		927	-----	926
Dd		963	GGCTCTGTGAAGHMAATCCTAGTCCTTACTGCTATTCTCAGCTTGTGTTACCT	1022
Qy		927	-----	926
Dd		1023	GTTGCCAACTTGGGCCAAACCGAATTTCTTTCCCAATCTTTAATTCTTGGCTGCAGCGAGAT	1082
Qy		927	----- --AGGAGCTGATCGACGAAATGGANNTGGTTATGCTGTAAATCCCAAGCAAT	976
Dd		1083	GTCCTCAACAAGBAGCTGATCGACAGAAATGGGANNTGGTTA-TGTGTTAAATGCCAGCAAT	1142
Qy		977	ACCTGTCCAAAGCCCTGACTTTATATCCCGAGTCTCAATTTCTCGTGCTGCTGTGAATGAC	1036
Dd		1143	ACCTGTCCAAAGCCCTGACTTTATCCCGAGTCTCAATTTCTCGTGCTGCTGTGAATGAC	1202
Qy		1037	AGCTTTTGTGAGAAATTTTCCCTGGTGTGGCAAAATTCAGTAGATTTCAATTGAGHAAGCA	1096
Dd		1203	AGCTTTTGTGAGAAATTTTCCCTGGTGTGGCAAAATTCAGTAGATTTCAATTGAGHAAGCA	1262
Qy		1097	AAAGCTCCAAATGGAATGTTTCTAGTCGCTGTTAGCTGGGATCTCCCGCTCCGCCACC	1156
Dd		1263	AAAGCTCCAAATGGAATGTTTCTAGTCGCTGTTAGCTGGGATCTCCCGCTCCGCCACC	1322
Qy		1157	ATCGTATCGCTACATCATGAAGAGATGGAATGTCTTTAGATGAAGCTTACAGATTT	1216
Dd		1323	ATCGTATCGCTACATCATGAAGAGATGGAATGTCTTTAGATGAAGCTTACAGATTT	1382

[illegible]

Qy	2297	GAGAGCATCATGTGCAGAGAAACAGGTCA	CGGGAAGAGCTGGGAAAGTGGGAGTCAGTCT	2355
Db	2463	GAGAGCATCATGTGCAGAGAAACAGGTCA	CGGGAAGAGCTGGGAAAGTGGGAGTCAGTCT	2522
Qy	2357	AGCTTTTTCGGGCAGCATGGAAATCATTTG	AGGTCTCTCTGAGAGAAAGACACTTGTGACTT	2416
Db	2523	AGCTTTTTCGGGCAGCATGGAAATCATTTG	AGGTCTCTCTGAGAGAAAGACACTTGTGACTT	2582
Qy	2417	CTATAGACAAATTTTTTTTTTTCTTGTTCA	CAAAAATAATTCCTCTAAATCTGAAATATATAT	2476
Db	2583	CTATAGACAAATTTTTTTTTTTCTTGTTCA	CAAAAATAATTCCTCTAAATCTGAAATATATAT	2642
Qy	2477	ATGTACATACATATATATTTTTTGGAAAT	TGGAAATGGAGCTATGTTGTAAAGCAACAGGTGGATC	2536
Db	2643	ATGTACATACATATATATTTTTTGGAAAT	TGGAAATGGAGCTATGTTGTAAAGCAACAGGTGGATC	2702
Qy	2537	AACCCAGTTTCTTACTCTCTTACATCTGCA	TATTTGAGATCAGCTATATCTTCTCTCAA	2595
Db	2703	AACCCAGTTTCTTACTCTCTTACATCTGCA	TATTTGAGATCAGCTATATCTTCTCTCAA	2762
Qy	2596	CAAAAATGGAAAGGCGAGATGCTAGAAAT	CCCCCTTAGACGGAGGAAAACCATTTTATTCAG	2655
Db	2763	CAAAAATGGAAAGGCGAGATGCTAGAAAT	CCCCCTTAGACGGAGGAAAACCATTTTATTCAG	2822
Qy	2656	TGAATTCACATCTCTTGTGTTCTTAAAGAG	CAAGTGCTTTGGTGGAGGACAAAT	2715
Db	2823	TGAATTCACATCTCTTGTGTTCTTAAAGAG	CAAGTGCTTTGGTGGAGGACAAAT	2882
Qy	2716	CCCTACCATTTCACAGTTGTGCTACTAAG	AGATCTCAAATATTAGTCTTTGTCCGAC	2775
Db	2883	CCCTACCATTTCACAGTTGTGCTACTAAG	AGATCTCAAATATTAGTCTTTGTCCGAC	2941
Qy	2776	CGTTCATAGTACACCTTAGCGGTGAGACTG	AGCCAGCTTGGGGTCAGGTAGGTAGACC	2835
Db	2942	CGTTCATAGTACACCTTAGCGGTGAGACTG	AGCCAGCTTGGGGTCAGGTAGGTAGACC	3001
Qy	2836	CTGTATGGGACAGAGCCTTAGTGTAAATCC	AAGAAAATGATCCTATCAAAGCTGATTC	2895
Db	3002	CTGTATGGGACAGAGCCTTAGTGTAAATCC	AAGAAAATGATCCTATCAAAGCTGATTC	3061
Qy	2896	ACAAACCCACGCTACCTGACAGCCGAGGGA	CACAGAGCATCACTCTGCTGGACGGACCAT	2955
Db	3062	ACAAACCCACGCTACCTGACAGCCGAGGGA	CACAGAGCATCACTCTGCTGGACGGACCAT	3121
Qy	2956	TAGGGGCTTCCAAAGTCTACCTTAGAGCAAA	CCAGTACCTCAGACAGGAAAAGTCGGG	3015
Db	3122	TAGGGGCTTCCAAAGTCTACCTTAGAGCAAA	CCAGTACCTCAGACAGGAAAAGTCGGG	3181
Qy	3016	GCTTTGACCACTACCATATCTGTAGCCCAAT	TTTCTTAGCCATTTGTGAATAGTAGGTAGC	3075
Db	3182	GCTTTGACCACTACCATATCTGTAGCCCAAT	TTTCTTAGCCATTTGTGAATAGTAGGTAGC	3241
Qy	3076	TAGTCACACTTTTCAGACCAATTCAAACTG	CTCTATGCAAAAATTCCTGTCGGGCTAGAT	3135
Db	3242	TAGTCACACTTTTCAGACCAATTCAAACTG	CTCTATGCAAAAATTCCTGTCGGGCTAGAT	3301
Qy	3136	GGAGTAAATTTTTTTTTTTCTCTCAGCTTT	TATGAGAGAGGGAACCTGCTAGATTCAG	3195
Db	3302	GGAGTAAATTTTTTTTTTTCTCTCAGCTTT	TATGAGAGAGGGAACCTGCTAGATTCAG	3361
Qy	3196	CTGAACCCACAGGAACCTGGCAACATCAGAT	TAAAGCTTAAGTTGGGAGGCTAACGAGT	3255
Db	3362	CTGAACCCACAGGAACCTGGCAACATCAGAT	TAAAGCTTAAGTTGGGAGGCTAACGAGT	3421
Qy	3256	CTACCTCCCTCTTTGTAATCAAGAAATGTT	TTTAAATGGATTTGTAATCTTTAAATA	3315
Db	3422	CTACCTCCCTCTTTGTAATCAAGAAATGTT	TTTAAATGGATTTGTAATCTTTAAATA	3481
Qy	3316	AAGATGAACCTTGGTTTC	3332	
Db	3482	AAGATGAACCTTGGTTTC	3498	

[illegible]

Db 601 GGAACGGAAAAAGTGTCTAATTGATAGCCGGCCATTGTGGAATACAAATACATCCAC 660
Qy 685 ATTTTGGAAAGCCATTAAATCAACTGCTCCAGCTTATGAAGCGAAGTTGCAACAGAC 744
Db 661 ATTTTGGAAAGCCATTAAATCAACTGCTCCAGCTTATGAAGCGAAGTTGCAACAGAC 720
Qy 745 AAAGTGTAAATACAGAGTCTATCCAGCATTCAGCGAAACATGAAGTTGACATTGATTC 804
Db 721 AAAGTGTAAATACAGAGTCTATCCAGCATTCAGCGAAACATGAAGTTGACATTGATTC 780
Qy 805 AGTCAGAAAGTTGATTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCTCTTCAGAC 864
Db 781 AGTCAGAAAGTTGATTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCTCTTCAGAC 840
Qy 865 TGTCTTCTCACTGCTACTCTCTGGTAACTGGAGAGAGCTTCAACTCTGTTCACTGCT 924
Db 841 TGTCTTCTCACTGCTACTCTCTGGTAACTGGAGAGAGCTTCAACTCTGTTCACTGCT 900
Qy 925 GC----- 926
Db 901 GCAGGTGGGTTTGTCTGAGTTCTCTCTGTTGTTTCCCTGGCCTCTGTGAAGGAAAAATCCACT 960
Qy 927 ----- 926
Db 961 CTAGTCCTTACCTGCAATTTCTCAGCCTTGTCTTACCTGTTGCCAATGTTGGGCCAACCCGA 1020
Qy 927 -----AGGAGCTGATGCAG 940
Db 1021 ATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGCTCTCAACAGAGCTGATGCAG 1080
Qy 941 CAGAAAGGGATTGGTATGTTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATC 1000
Db 1081 CAGAAAGGGATTGGTATGTTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATC 1140
Qy 1001 CCCGAGTCTCATTTCTCTGCTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCG 1060
Db 1141 CCCGAGTCTCATTTCTCTGCTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCG 1200
Qy 1061 TGGTTGGACAAATCAGTAGATTTTATGAGAAAGCAAAAGCCTCCAAATGGATGTTCTTA 1120
Db 1201 TGGTTGGACAAATCAGTAGATTTTATGAGAAAGCAAAAGCCTCCAAATGGATGTTCTTA 1260
Qy 1121 GTGCACATGTTTAGTGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAAG 1180
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Qy 1181 AGGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAGACCTACTATA 1240
Db 1321 AGGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAGACCTACTATA 1380
Qy 1241 TCTCCAACTTCAATTTTCTGGGCCACTCTGACTATGAGAGAGATTAAGAACCG 1300
Db 1381 TCTCCAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAGAGATTAAGAACCG 1440
Qy 1301 ACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGGCCAAATGAA 1360
Db 1441 ACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGGCCAAATGAA 1500
Qy 1361 CCTGTCCCTGTCTGTCTCAGAGGTGGACAGAAAAGGAGACGCCCTCAGTCCACCTGT 1420
Db 1501 CCTGTCCCTGTCTGTCTCAGAGGTGGACAGAAAAGGAGACGCCCTCAGTCCACCTGT 1560
Qy 1421 GCCGACTCTGCTACTCTCAGAGGCGAGGACAAAGCCCGTGATCCCGCCAGCGTGCCC 1480
Db 1561 GCCGACTCTGCTACTCTCAGAGGCGAGGACAAAGCCCGTGATCCCGCCAGCGTGCCC 1620
Qy 1481 AGCGTGCCAGCGTGACCGCTGCTGTTTAGAGAGACAGCCCGCTGTGTAAGGGCTCAGT 1540
Db 1621 AGCGTGCCAGCGTGACCGCTGCTGTTTAGAGAGACAGCCCGCTGTGTAAGGGCTCAGT 1680
Qy 1541 GGGCTGCACTGTCTCCGAGAGCGCTGGAGAGACAGCAATAGCTCAAGCGTTCTCTCT 1600
Db 1681 GGGCTGCACTGTCTCCGAGAGCGCTGGAGAGACAGCAATAGCTCAAGCGTTCTCTCTCT 1740

Qy 1601 CTGGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTTACATGGCTTCTCC 1660
Db 1741 CTGGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTTACATGGCTTCTCC 1800
Qy 1661 TCATCAGAAGATGCTTTTGGAAATCTACAAAACCTTCCACTACTCTGATGGGACCAACAG 1720
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Qy 1721 CTATGCCAGTTCTCCCTGTTTCAGAACTATCGGAGCAGACTCCCGAAACAGTCTCTGAT 1780
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Qy 1781 AAGGAGGAGCCAGCATCCCAAGAGCTGCAGACCCGACAGCCTTCAGACAGCCAGC 1840
Db 1921 AAGGAGGAGCCAGCATCCCAAGAGCTGCAGACCCGACAGCCTTCAGACAGCCAGC 1980
Qy 1841 AAGCGATTCATTCGCTCAGAACCCAGCAGCAGTGCACCCGCGCAGAGGTCCTTTTATCT 1900
Db 1981 AAGCGATTCATTCGCTCAGAACCCAGCAGCAGTGCACCCGCGCAGAGGTCCTTTTATCT 2040
Qy 1901 CCACTGCTATCGAAGTGGGAGCGTGGAGGACAAATTAACCAACCAAGCTTCCTTTTCGGCCTT 1960
Db 2041 CCACTGCTATCGAAGTGGGAGCGTGGAGGACAAATTAACCAACCAAGCTTCCTTTTCGGCCTT 2100
Qy 1961 TCACAGCAGCAGCAGCATCTCAGAACTCTGCTGGCCTTAAAGGCTGGCACTCG 2020
Db 2101 TCACAGCAGCAGCAGCATCTCAGAACTCTGCTGGCCTTAAAGGCTGGCACTCG 2160
Qy 2021 GATATCTGGCCCCCAGACCTCTACCCCTTCCCTGACACAGCAGCTGTAATTTTGCACA 2080
Db 2161 GATATCTGGCCCCCAGACCTCTACCCCTTCCCTGACACAGCAGCTGTAATTTTGCACA 2220
Qy 2081 GAGTCTCTACATTTCTCTGCTCAGCATCTACGGAGCAGTGCCTTACTCTGCTCC 2140
Db 2221 GAGTCTCTACATTTCTCTGCTCAGCATCTACGGAGCAGTGCCTTACTCTGCTCC 2280
Qy 2141 TACAGCTGAGCAGCAGCTGCCACTTTCGGAGACCAAGTCTATTCTGTGCGCAGCGGCGAG 2200
Db 2281 TACAGCTGAGCAGCAGCTGCCACTTTCGGAGACCAAGTCTATTCTGTGCGCAGCGGCGAG 2340
Qy 2201 AAGCCAAAGTGACAGAGCTGACTTCGCGCGGAGCTGGCATGAAGAGAGCCCTTTGAAAAG 2260
Db 2341 AAGCCAAAGTGACAGAGCTGACTTCGCGCGGAGCTGGCATGAAGAGAGCCCTTTGAAAAG 2400
Qy 2261 CAGTTTAAACGAGAGCTGCCAAATGGAATTTGGAGAGCATCATGTCTCAGAGAACAGG 2320
Db 2401 CAGTTTAAACGAGAGCTGCCAAATGGAATTTGGAGAGCATCATGTCTCAGAGAACAGG 2460
Qy 2321 TCACGGAAAGAGCTGGGAAAGTGGGCGAGTCTAGCTTTTCGGGCGAGCATGGAAATC 2380
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Qy 865 TGTGTTCTCACTGTACTCTCGGTTAACTGAGAGAGAGCTCAACTCTGTTTCACTGCTT 924
Db 841 TGTGTTCTCACTGTACTCTCGGTTAACTGAGAGAGAGCTCAACTCTGTTTCACTGCTT 900
Qy 925 GC----- 926
Db 901 GAGGTGGGTTGCTGAGTCTCTCTGTTGTTTCCCTGGCTCTGTGAAGGAATAATCCACT 960
Qy 927 ----- 926
Db 961 CTAGTCCCTACCTGCAATTTCTCAGCGCTTCTTACCTGTTGCTGCAATTTGGGCCAACCCGA 1020
Qy 927 -----AGGAGCTGATCGAG 940
Db 1021 ATTCTTCCCAATCTTATCTTGCTGCCAGCAGATGTCCTCAACAGGAGCTGATACAG 1080
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AUTHORS
Todderud, C.G., Bol, D.,

Suchard, S., Banas, D., B.
Mcatee, P., Mintier, G.,

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1245	TCATGAAGAGGATGGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC	1300	
1233	CTACTATATCTCCAAACCTTCAATTTTCTGGGCAACTCTCGACTATGAGAGAAAGATTA	1299	
1305	CTACTATATCTCCAACTTCAATTTTCTGGGCAACTCTCGACTATGAGAGAAAGATTA	1366	
1293	AGAACACAGACTGGAGCATCAGGSCCAAAGAGCAAACTCAAGCTCTGCTCAGCTGGAGAGC	1355	
1365	AGAACACAGACTGGAGCATCAGGSCCAAAGAGCAAACTCAAGCTCTGCTCAGCTGGAGAGC	1422	
1353	CAAATGAACCTGTCCCTGTGCTCTCAGAGGGTGGACAGAAAAAGCGACAGCCCTCAGCTC	1411	
1425	CAAATGAACCTGTCCCTGTGCTCTCAGAGGGTGGACAGAAAAAGCGACAGCCCTCAGCTC	1480	
1413	CACCTGTGCGACTGTGCTACTCTAGAGCGAGCAGAGCAAAAGCCGTGCTATCCCGCCA	1472	
1485	CACCTGTGCGACTGTGCTACTCTAGAGCGAGCAGAGCAAAAGCCGTGCTATCCCGCCA	1540	
1473	GGTGCCACAGCTGCCAGGCTGACGCGCTGCTGTTAGAGGACAGCCCTGGTACAGG	1533	
1545	GGTGCCACAGCTGCCAGGCTGACGCGCTGCTGTTAGAGGACAGCCCTGGTACAGG	1600	
1533	CGCTCAGTGGACTGCACTCTGCGCAGACAGAGCTGGAAGACAGCAATTAAGCTCAAGCGTT	1599	
1605	CGCTCAGTGGACTGCACTCTGCGCAGACAGAGCTGGAAGACAGCAATTAAGCTCAAGCGTT	1666	
1593	CTTCTCTCTGGATATCAATTCAGTTTCTATTTAGCCAGCATGGCAGCATCTTACATG	1655	
1665	CTTCTCTCTGGATATCAATTCAGTTTCTATTTAGCCAGCATGGCAGCATCTTACATG	1722	
1653	GCTTCTCTCATCAGAAAGATGCTTTGGAATACTACAACCTTCCACTCTCTGGATGGGA	1711	
1725	GCTTCTCTCATCAGAAAGATGCTTTGGAATACTACAACCTTCCACTCTCTGGATGGGA	1780	
1713	CCAAACAGCTATGCCAGTTCTCCCTGTTTCAGGAATATCGGACAGACTCCCGGAAACCA	1777	
1785	CCAAACAGCTATGCCAGTTCTCCCTGTTTCAGGAATATCGGACAGACTCCCGGAAACCA	1840	
1773	GTCTGTATAGAGGAAAGCAAGATCCCAAGAGCTGCAGACCGCAGGCTTTCAGACA	1830	
1845	GTCTGTATAGAGGAAAGCAAGATCCCAAGAGCTGCAGACCGCAGGCTTTCAGACA	1900	
1833	GCCAGACAGACGATTCGATTTCCGTTCAAGAACAGCAGCAGTGGGACCGCCAGAGTGCC	1899	

[illegible]

Db	2984	CTGACAGCCGAGGACACGAGCATCACTCTGCTGGACGGACCAATTAGGGGGCTTGCCAG	3043
QY	2972	GTCTACCTTAGAGCAACCCAGTACCTCAGACAGAGAAAGTCGGGGCTTTTGACCACTACCA	3031
Db	3044	GTCTACCTTAGAGCAACCCAGTACCTCAGACAGAGAAAGTCGGGGCTTTTGACCACTACCA	3103
QY	3032	TATCTGGTAGCCATTTCTTAGGCATTTGTAATAGTAGTAGGTAGCTAGTCACACATTTTCAG	3091
Db	3104	TATCTGGTAGCCATTTCTTAGGCATTTGTAATAGTAGTAGGTAGCTAGTCACACATTTTCAG	3163
QY	3092	ACCAATTCAAACCTGTCTATGACCAAAAATCCCGTGGGCTAGATGGAGATAATTTTTTT	3151
Db	3164	ACCAATTCAAACCTGTCTATGACCAAAAATCCCGTGGGCTAGATGGAGATAATTTTTTT	3223
QY	3152	TCTTCTCAGCTTTATGAGAGAGAGGAAACTGCTTAGAGTTCAGCTGAACCAACCAAGAAC	3211
Db	3224	TCTTCTCAGCTTTATGAGAGAGAGGAAACTGCTTAGAGTTCAGCTGAACCAACCAAGAAC	3283
QY	3212	CTGGCAACATCAGATTTAAGCTTAAGCTTGGGAGGCTAACGAGTCTACTCCCTCTTTTGT	3271
Db	3284	CTGGCAACATCAGATTTAAGCTTGGGAGGCTAACGAGTCTACTCCCTCTTTTGT	3343
QY	3272	AAATCAAGAATTTGTTTAAATCGGATTCCTCAATCCTTTAAATAAAGATGAACCTTGGTTT	3331
Db	3344	AAATCAAGAATTTGTTTAAATCGGATTCCTCAATCCTTTAAATAAAGATGAACCTTGGTTT	3403
QY	3332	C 3332	
Db	3404	C 3404	
RESULT 10			
BC042101			
LOCUS			
DEFINITION	BC042101	2884 bp mRNA linear	PRI 07-OCT-2003
ACCESSION	MG:50665 IMAGE:4400999	complete cds.	
VERSION	BC042101.1	GI:27469788	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PubMed			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			

Db 1141 TTACAGATTTGTGAAGAAAGAAAGAACTTACTATATCTCCAAACTTTCANATTTCTGGGCCA 1200
QY 1267 ACTCCTCGACTATGAGAAGAAAGATTAAAGACAGACTGGAGCATCAGGGCCAAAGAGCAA 1326
Db 1201 ACTCCTCGACTATGAGAAGAAAGATTAAAGACAGACTGGAGCATCAGGGCCAAAGAGCAA 1260
QY 1327 ACTAAGCTGTGCACTCGGAGAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGG 1386
Db 1261 ACTAAGCTGTGCACTCGGAGAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGG 1320
QY 1387 ACAGAAAAGCAGAGCGCCCTCAGTCCACCCCTGTGCGGACTCTGCTACCTCAGAGGCAGC 1446
Db 1321 ACAGAAAAGCAGAGCGCCCTCAGTCCACCCCTGTGCGGACTCTGCTACCTCAGAGGCAGC 1380
QY 1447 AGGACAAAGCCCGTGCATCCGCCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCGCT 1506
Db 1381 AGGACAAAGCCCGTGCATCCCG-----CCAGCGTCCCGAGCGTCCAGCGTCCGCT 1431
QY 1507 GTTAGGAGACCGCGCTGGTACAGCGCTCAGTGGGCTGCACCTGTCCCGCAGCAGCGCT 1566
Db 1432 GTTAGGAGACCGCGCTGGTACAGCGCTCAGTGGGCTGCACCTGTCCCGCAGCAGCGCT 1491
QY 1567 GGAAGCAGCAATAGCTCAAGCGTTCCTTCTCTGATATCAATCAGTTCATATTC 1626
Db 1492 GGAAGCAGCAATAGCTCAAGCGTTCCTTCTCTGATATCAATCAGTTCATATTC 1551
QY 1627 AGCCAGCTGGCAGCATCTTACATGGTCTCTCTCATCAGAAGATGCTTTGGAACTA 1686
Db 1552 AGCCAGCTGGCAGCATCTTACATGGTCTCTCTCATCAGAAGATGCTTTGGAACTA 1611
QY 1687 CAAACCTTCCACTACTCTGGATGGACCAACAAAGCTATGCCAGTTCCTCCCTGTTCAGGA 1746
Db 1612 CAAACCTTCCACTACTCTGGATGGACCAACAAAGCTATGCCAGTTCCTCCCTGTTCAGGA 1671
QY 1747 ACTATCGGAGCAGACTCCGAAACAGTCTCTGATAGGAGAGCCAGCATCCCAAGAA 1806
Db 1672 ACTATCGGAGCAGACTCCGAAACAGTCTCTGATAGGAGAGCCAGCATCCCAAGAA 1731
QY 1807 GCTGCAGACCGCCAGCGCTTCAGACGCGCAGAGCAGCGATTCGGTTCAGAACAG 1866
Db 1732 GCTGCAGACCGCCAGCGCTTCAGACGCGCAGAGCAGCGATTCGGTTCAGAACAG 1791
QY 1867 CAGCAGTGGCAGCGCCAGAGTCCCTTTATCTCCACTGCATCGAAGTGGAGCGTGA 1926
Db 1792 CAGCAGTGGCAGCGCCAGAGTCCCTTTATCTCCACTGCATCGAAGTGGAGCGTGA 1851
QY 1927 GGAACAATTACCAACAGCTTCCTTTTCGCGCTTTTCCACAGCCAGCAGCACCTCAGGAA 1986
Db 1852 GGAACAATTACCAACAGCTTCCTTTTCGCGCTTTTCCACAGCCAGCAGCACCTCAGGAA 1911
QY 1987 GTCTGTGGCTGGGCTTAAAGGCTGGCACTCGGATATCTGGCGCCCGCAGACCTCTAC 2046
Db 1912 GTCTGTGGCTGGGCTTAAAGGCTGGCACTCGGATATCTGGCGCCCGCAGACCTCTAC 1971
QY 2047 CCCTTCCCTCAGCAGCAGCTGTATTTTGCACAGAGTCTCACAACCTTCTACTCTGCGCTC 2106
Db 1972 CCCTTCCCTCAGCAGCAGCTGTATTTTGCACAGAGTCTCACAACCTTCTACTCTGCGCTC 2031
QY 2107 AGCCATCTACGGAGGCACTGCCAGTTCCTCTGCTCAGTGCAGCAGCTGCCCACTTG 2166
Db 2032 AGCCATCTACGGAGGCACTGCCAGTTCCTCTGCTCAGTGCAGCAGCTGCCCACTTG 2091
QY 2167 CGGAGCCAGTCTATCTGTGCGAGCGGAGAGCCAGTGCAGAGCTGACTCGCG 2226
Db 2092 CGGAGCCAGTCTATCTGTGCGAGCGGAGAGCCAGTGCAGAGCTGACTCGCG 2151
QY 2227 GCGAGCTGGCAGAGAGCCCTTTGAAAGCAGTTCATTAACGAGAGCTGCCAAAT 2286
Db 2152 GCGAGCTGGCAGAGAGCCCTTTGAAAGCAGTTCATTAACGAGAGCTGCCAAAT 2211
QY 2287 GGAATTTGGAGAGCATCATGTACAGACAGCTCAGCGAGAGCTCGCGAAAGTGGG 2346

RESULT 11
BD171157

Db 2212 GGAATTTGGAGAGAGCATCATGTACAGAAACAGGTCAACGGAAGAGCTGGGAAAAGTGGG 2271
QY 2347 CAGTCAGTCTAGCTTTTCGGGAGCATGGAATCATTTGAGTCTCTCTGAGAGCAAGAGACA 2406
Db 2272 CAGTCAGTCTAGCTTTTCGGGAGCATGGAATCATTTGAGTCTCTCTGAGAGCAAGAGACA 2331
QY 2407 CTCTGACTCTCTATAGACAATTTTTTTTCTTCTTCAAAAAAATTCCTGTAAATCTG 2466
Db 2332 CTCTGACTCTCTATAGACAATTTTTTTTCTTCTTCAAAAAAATTCCTGTAAATCTG 2391
QY 2467 AAATATATATGTACATATATATTTTGGAAAATGGAGCTATGTTGTAAGAGCAA 2526
Db 2392 AAATATATATGTACATATATATTTTGGAAAATGGAGCTATGTTGTTAAAGCAA 2451
QY 2527 CAGTGGATCAACCCAGTGTACTCTCTTAAACATCTGCAATTTGAGAGATCAGCTAATAC 2586
Db 2452 CAGTGGATCAACCCAGTGTACTCTCTTAAACATCTGCAATTTGAGAGATCAGCTAATAC 2511
QY 2587 TTCTCTCAAAAAATGGAAGGAGATGTAGATCCCTCTAGAGCGGAGGAAAACCAT 2646
Db 2512 TTCTCTCAAAAAATGGAAGGAGATGTAGATCCCTCTAGAGCGGAGGAAAACCAT 2571
QY 2647 TTATTTCAGTCAATTAACATCTCTTCTTAAAAAAGCAAGTGTCTTTGGTGTGGA 2706
Db 2572 TTATTTCAGTCAATTAACATCTCTTCTTAAAAAAGCAAGTGTCTTTGGTGTGGA 2631
QY 2707 GGAACAAATCCCTTACCAATTTTCCAGTGTGTCTTAAAGAGATCTCAATATATAGTCTT 2766
Db 2632 GGAACAAATCCCTTACCAATTTTCCAGTGTGTCTTAAAGAGATCTCAATATATAGTCTT 2690
QY 2767 TGTCGGAGCCCTTCCATAGTACACTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGT 2826
Db 2691 TGTCGGAGCCCTTCCATAGTACACTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGT 2750
QY 2827 AGGTAGACCTCTTTAGGAGACAGAGCTAGTGTAAATCCAGAGAAATGATCTATCCAA 2886
Db 2751 AGGTAGACCTCTTTAGGAGACAGAGCTAGTGTAAATCCAGAGAAATGATCTATCCAA 2810
QY 2887 AGCTGATTCACAAACCCAGCTCACCTGACAGCGAGGACACAGAGCATCACTCTGCTGG 2946
Db 2811 AGCTGATTCACAAACCCAGCTCACCTGACAGCGAGGACACAGAGCATCACTCTGCTGG 2870
QY 2947 ACGGACCAATTAGGGGCTTGCCAAAGTCTACCTTAGAGCAAAACCCAGTACTCAGACAGG 3006
Db 2871 ACGGACCAATTAGGGGCTTGCCAAAGTCTACCTTAGAGCAAAACCCAGTACTCAGACAGG 2930
QY 3007 AAAGTCGGGCTTTGACCACTACCATATCTGTAGCCCATTTCTAGGCATTTGTGAATAG 3066
Db 2931 AAAGTCGGGCTTTGACCACTACCATATCTGTAGCCCATTTCTAGGCATTTGTGAATAG 2990
QY 3067 GTAGGTAGCTAGTCAACCTTTTTCAGACCAATTCAAAACCTGTCTATGCAAAAATTCCTG 3126
Db 2991 GTAGGTAGCTAGTCAACCTTTTTCAGACCAATTCAAAACCTGTCTATGCAAAAATTCCTG 3050
QY 3127 GGCCTAGATGGAGATAATTTTTTTTCTCTCAGCTTTATGAAGAGAGGAAACTGTCT 3186
Db 3051 GGCCTAGATGGAGATAATTTTTTTTCTCTCAGCTTTATGAAGAGAGGAAACTGTCT 3110
QY 3187 AGGATTCAGCTCAACCCAGGAACTTCGCAACATCACGATTTAAGCTTAAGCTTGGGAGG 3246
Db 3111 AGGATTCAGCTCAACCCAGGAACTTCGCAACATCACGATTTAAGCTTAAGCTTGGGAGG 3170
QY 3247 CTAAAGCTTACCTCCCTCTTGTAAATCAAGAAATTTTAAATGGGATTTGTCAATC 3306
Db 3171 CTAAAGCTTACCTCCCTCTTGTAAATCAAGAAATTTTAAATGGGATTTGTCAATC 3230
QY 3307 CTTTAAATAAGATGAATCTGTTTC 3332
Db 3231 CTTTAAATAAGATGAATCTGTTTC 3256

LOCUS	BD171157	Novel gene	4790 bp	DNA	linear	PAT 17-JAN-2003
DEFINITION	Novel gene and protein encoded thereby.					
ACCESSION	BD171157					
VERSION	BD171157.1	GI:27876969				
KEYWORDS	WO 02052005-A/13.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 4790)					
AUTHORS	Ohara,O., Nagase,T. and Nakajima,D.					
TITLE	Novel gene and protein encoded thereby					
JOURNAL	Patent: WO 02052005-A 13 04-JUL-2002; KAZUSA DNA RESEARCH INSTITUTE,OSAMU OHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIMA					
COMMENT	OS Homo sapiens (human) PN WO 02052005-A/13 PD 04-JUL-2002 PF 20-DEC-2001 WO 2001JP011217 PR 22-DEC-2000 JP OOP 389742 PI OSAMU OHARA,TAKAHIRO NAGASE,DAISUKE NAKAJIMA PC CL2N15/12,C07K14/47 CC Novel gene and protein encoded thereby FH Location/Qualifiers FT CDS (184)..(2178).					
FEATURES	Location/Qualifiers 1..4790 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"					
ORIGIN	Query Match 83.0%; Score 2766.4; DB 6; Length 4790; Best Local Similarity 94.7%; Pred. No. 0; Matches 2952; Conservative 0; Mismatches 1; Indels 165; Gaps 2;					
QY	379	GAAGAAGACATTACCTTTGAGGGCTCTTCTGCTGAAATGGTTTAACTCTCTTTTGGCAG	438			
DB	1	GAAGAAGACATTACCTTTGAGGGCTCTTCTGCTGAAATGGTTTAACTCTCTTTTGGCAG	60			
QY	439	TCACCAACCGCTGACCTCATACACCTTTTGTACAAATGAGTGGCTGAGCTTTGAGCAC	498			
DB	61	TCACCAACCGCTGACCTCATACACCTTTTGTACAAATGAGTGGCTGAGCTTTGAGCAC	120			
QY	499	ACCACATTACATCATCTGTCGCAAAATTAAGAAGGAGGTGGGAAAGAGGACTTATTGTT	558			
DB	121	ACCACATTACATCATCTGTCGCAAAATTAAGAAGGAGGTGGGAAAGAGGACTTATTGTT	180			
QY	559	GTCATGCCCATCAGATGATTGGAACCTCAAAATGTTTACTGAGAGGTGGTGGCTCTGCTG	618			
DB	181	GTCATGCCCATCAGATGATTGGAACCTCAAAATGTTTACTGAGAGGTGGTGGCTCTGCTG	240			
QY	619	GAAGTGGAAAGCAAAAGTGTCTTAATGTAGTACCGGCCATTGTTGGAATACAAATACA	678			
DB	241	GAAGTGGAAAGCAAAAGTGTCTTAATGTAGTACCGGCCATTGTTGGAATACAAATACA	300			
QY	679	TCCCAACATTTTGAAGCCATTAAATATCACTGCTCCAGCTTATGAAGGAGGTGCAA	738			
DB	301	TCCCAACATTTTGAAGCCATTAAATATCACTGCTCCAGCTTATGAAGGAGGTGCAA	360			
QY	739	CAGGACAAAGTGTAAATACAGAGCTCATCCAGCTTATCAGCAAAACATAAGGTTCACATT	798			
DB	361	CAGGACAAAGTGTAAATACAGAGCTCATCCAGCTTATCAGCAAAACATAAGGTTCACATT	420			
QY	799	GATTGCACTCAGAAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTCT	858			
DB	421	GATTGCACTCAGAAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTCT	480			
QY	859	TCGACATGTTTTCTCACTGTACTTCTGGGTAACTGGGAGAGGCTTCAACTCTGTTCCAC	918			
DB	481	TCGACATGTTTTCTCACTGTACTTCTGGGTAACTGGGAGAGGCTTCAACTCTGTTCCAC	540			
QY	919	CTGCTTTCG-----	926			

Db	1621	CAGACGAAGCGAATTGGCATTCGGTCAGAACCAAGCAGCAGTGGCGACCGCCGACGAGTGCCTTT	1680
Qy	1895	TTATCTCCACTGTCATCGAAGTGGGAGCGTGGAGGACAAATTACCAACACAGCTTCCTTTTTC	1954
Db	1681	TTATCTCCACTGTCATCGAAGTGGGAGCGTGGAGGACAAATTACCAACACAGCTTCCTTTTTC	1740
Qy	1955	GGCCTTTTCCACGCGCAGCAGCACCTTCACGAGTCTGTGGCTGGGCTTAAAGGCTGG	2014
Db	1741	GGCCTTTTCCACGCGCAGCAGCACCTTCACGAGTCTGTGGCTGGGCTTAAAGGCTGG	1800
Qy	2015	CACCTCGGATATCTTGGGCCCCCCAGACGCTCTACCCCTTCCTCACCAGCAGCTGGTATTTT	2074
Db	1801	CACCTCGGATATCTTGGGCCCCCCAGACGCTCTACCCCTTCCTCACCAGCAGCTGGTATTTT	1860
Qy	2075	GGCCACAGAGTCTCTACAGTCTTACTCTGGCTCAGCCATCTACGGAGGAGTGCACAGTTAC	2134
Db	1861	GGCCACAGAGTCTCTACAGTCTTACTCTGGCTCAGCCATCTACGGAGGAGTGCACAGTTAC	1920
Qy	2135	TCCTGCTACAGCTGCAGCCAGCTGCCACCTTGGCGAGACCAAGTCTATCTGTGCGCAGG	2194
Db	1921	TCCTGCTACAGCTGCAGCCAGCTGCCACCTTGGCGAGACCAAGTCTATCTGTGCGCAGG	1980
Qy	2195	CGGCGAAGCCAAAGTGCACAGATGACCTCGCGCGGAGCTGGCGATGGAAGAGGCCCCCTTT	2254
Db	1981	CGGCGAAGCCAAAGTGCACAGATGACCTCGCGCGGAGCTGGCGATGGAAGAGGCCCCCTTT	2040
Qy	2255	GAAAGCAGTCTTAAAGCCAGAAAGCTGCCAAATCGMAATTTGGAGAGAGCATCATCTCAGAG	2314
Db	2041	GAAAGCAGTCTTAAAGCCAGAAAGCTGCCAAATCGMAATTTGGAGAGAGCATCATCTCAGAG	2100
Qy	2315	AACAGGTCACGGGAAAGCTGGGGAAAGTGGGCAAGTCAGTCTAGCTTTTCGGGCAAGCATG	2374
Db	2101	AACAGGTCACGGGAAAGCTGGGGAAAGTGGGCAAGTCAGTCTAGCTTTTCGGGCAAGCATG	2160
Qy	2375	GAAATCATTTGAGGTCTCCTGGAAGAAGAAGACACTTGTGACTTCTATAGACAAATTTTTTTT	2434
Db	2161	GAAATCATTTGAGGTCTCCTGGAAGAAGAAGACACTTGTGACTTCTATAGACAAATTTTTTTT	2220
Qy	2435	TCCTGCTCACAAAAAATTCCTCTGAATCTCGAAATATATATATGTACATACATATATAT	2494
Db	2221	TCCTGCTCACAAAAAATTCCTCTGAATCTCGAAATATATATATGTACATACATATATAT	2380
Qy	2495	TTTTGGAAAAATGGAGCTATGTGTAAAGCAACAGGTGGATCAACCCAGTTGTTACTCTC	2554
Db	2281	TTTTGGAAAAATGGAGCTATGTGTAAAGCAACAGGTGGATCAACCCAGTTGTTACTCTC	2340
Qy	2555	TTAAATCTGCATTTAGAGATCAGCTAAATACCTTCTCAACAAAAATGGGAAGGCGAGAT	2614
Db	2341	TTAAATCTGCATTTAGAGATCAGCTAAATACCTTCTCAACAAAAATGGGAAGGCGAGAT	2400
Qy	2615	GCTAGATCCCCCTTAGACGGAGGAAAAACCATTTTATTCAGTGAATTACATCCTCTTG	2674
Db	2401	GCTAGATCCCCCTTAGACGGAGGAAAAACCATTTTATTCAGTGAATTACATCCTCTTG	2460
Qy	2675	TTCTTAAAAAAGCAGTGTCTTTGGTGTGGAGGACAAATCCCTTACCATTTTCCAGT	2734
Db	2461	TTCTTAAAAAAGCAGTGTCTTTGGTGTGGAGGACAAATCCCTTACCATTTTCCAGT	2519
Qy	2735	TGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGGAACCTTCCATAGTACACCTTA	2794
Db	2520	TGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGGAACCTTCCATAGTACACCTTA	2579
Qy	2795	GGCTGAGACTGAGCCAGCTTTGGGGGTACGTTAGGTAGTACCCCTGTTTAGGGACAGAGCCCTA	2854
Db	2580	GGCTGAGACTGAGCCAGCTTTGGGGGTACGTTAGGTAGTACCCCTGTTTAGGGACAGAGCCCTA	2639
Qy	2855	GTGGTAAATCCAAAGAGAAATCATCTTATCCAAAGCTGATTTCAAAACCCACGCTCACCTG	2914
Db	2640	GTGGTAAATCCAAAGAGAAATCATCTTATCCAAAGCTGATTTCAAAACCCACGCTCACCTG	2699
Qy	2915	ACAGCCGAGGGACACGAGCATCACTCTGCTGGAACCAATTAGGGGCTTTGCCAAGTCT	2974
Db	2700	ACAGCCGAGGGACACGAGCATCACTCTGCTGGAACCAATTAGGGGCTTTGCCAAGTCT	2759

[illegible]

Db 121 ACCACCAATTACATCATCGTGCAAAATTAAGAGAGGAGGTGGGAAAGAGACTTAATGTT 180
Qy 559 GTCATGGCCCATGAGATGGAATGGAACCAAAATGTTACTGAGAGGTTGGTGGCTCTGCTG 618
Db 181 GTCATGGCCCATGAGATGGAATGGAACCAAAATGTTACTGAGAGGTTGGTGGCTCTGCTG 240
Qy 619 GAAAGTGGAAACGGAAGAAAGTCTGCTAAATGATAGCCGCGCATTTGTGGAATACAATACA 678
Db 241 GAAAGTGGAAACGGAAGAAAGTCTGCTAAATGATAGCCGCGCATTTGTGGAATACAATACA 300
Qy 679 TCCACACATTTTGGAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGCAAA 738
Db 301 TCCACACATTTTGGAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGCAAA 360
Qy 739 CAGGACAAAGTGTAAATACAGAGCTCATCCAGCAATTCAGCGAAAATAAGGTTGACATT 798
Db 361 CAGGACAAAGTGTAAATACAGAGCTCATCCAGCAATTCAGCGAAAATAAGGTTGACATT 420
Qy 799 GATTGCGATCAGAGGTTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCT 858
Db 421 GATTGCGATCAGAGGTTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCTCT 480
Qy 859 TCAGACTGTTTCTCACTGACTCTCTGGGTAATCGAGAGAGCTTCAACTCTGTTTCA 918
Db 481 TCAGACTGTTTCTCACTGACTCTCTGGGTAATCGAGAGAGCTTCAACTCTGTTTCA 540
Qy 919 CTGCTTGC----- 926
Db 541 CTGCTTGCAGGTGGTGTGAGTTCCTCGTGTGTTTCCCTGGGCTCTGTGAAGAAAA 600
Qy 927 ----- 926
Db 601 TCCACTCTAGTCCCTACCTGCAATTCAGCCITTGCTTAACCTGTGCGCAACATGGGCA 660
Qy 927 -----AGAGCTG 934
Db 661 ACCCGAATTTCCCAATCTTTATCTTGGCTGCCAGCAGATGCTCAACAGGAGCTG 720
Qy 935 ATGCAGCAGAAATGGATGGTATGCTTAAATGCGAGCAATACCTGTCCAAAGCCTGAC 994
Db 721 ATGCAGCAGAAATGGATGGTATGCTTAAATGCGAGCAATACCTGTCCAAAGCCTGAC 780
Qy 995 TTTATCCCGAGTCTCATTTCTCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAAAT 1054
Db 781 TTTATCCCGAGTCTCATTTCTCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAAAT 840
Qy 1055 TTGCGGTGGTGGACAAATCAGTAGATTTTCATTTGAGAAAGCAAAAGCCCTCCATGGATGT 1114
Db 841 TTGCGGTGGTGGACAAATCAGTAGATTTTCATTTGAGAAAGCAAAAGCCCTCCATGGATGT 900
Qy 1115 GTTCTAGTGCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCACCATTCGCTTACATC 1174
Db 901 GTTCTAGTGCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCACCATTCGCTTACATC 960
Qy 1175 ATGAAGAGGATGGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCT 1234
Db 961 ATGAAGAGGATGGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCT 1020
Qy 1235 ACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGACTATCAGAAAGAAATTAAG 1294
Db 1021 ACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGACTATCAGAAAGAAATTAAG 1080
Qy 1295 AACCAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTCGAGAGGCA 1354
Db 1081 AACCAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTCGAGAGGCA 1140
Qy 1355 AATGAACTGTCCCTGTGCTCAGAGGGTGGACAGAAAGCGAGAGCGCCCTCAGTCCA 1414
Db 1141 AATGAACTGTCCCTGTGCTCAGAGGGTGGACAGAAAGCGAGAGCGCCCTCAGTCCA 1200
Qy 1415 CCCTGTGCCGACTCTGCTACCTCAGAGGCGAGGCAAAAGGCCCGCTGATCCCGCAGC 1474

Db 1201 CCCTGTGCCGACTCTGCTACCTCAGAGGCGAGCGAGCAAAAGGCCCGTGCATCCCGCCAGC 1260
Qy 1475 GTGCCACGCGTGGCCAGCGCTGACGCGTGGCTGTGTAGAGGACAGCCGCTGTGTACAGGCG 1534
Db 1261 GTGCCACGCGTGGCCAGCGTGCAGCGTGCCTGTGTAGAGGACAGCCGCTGTGTACAGGCG 1320
Qy 1535 CTCACTGGGCTGCACCTGTCCGAGAGCAGCGCTGGAAAGACAGCAATAAGCTCAAGGTTCC 1594
Db 1321 CTCACTGGGCTGCACCTGTCCGAGAGCAGCGCTGGAAAGACAGCAATAAGCTCAAGGTTCC 1380
Qy 1595 TTCTCTCTGATATCAAACTCAGTTTCATATTCAGCCAGCATGGCAGCATCTTATCATGGC 1654
Db 1381 TTCTCTCTGATATCAAACTCAGTTTCATATTCAGCCAGCATGGCAGCATCTTATCATGGC 1440
Qy 1655 TTCTCTCTCATCAGAGATGCTTGGAAATCTAATAACCTTCCACTCTCTGATGGGACC 1714
Db 1441 TTCTCTCTCATCAGAGATGCTTGGAAATCTAATAACCTTCCACTCTCTGATGGGACC 1500
Qy 1715 AACAACTATGCGCAGTCTTCCCTGTTCAGGAACATTCGAGCAGACTCCCGAAACCACT 1774
Db 1501 AACAACTATGCGCAGTCTTCCCTGTTCAGGAACATTCGAGCAGACTCCCGAAACCACT 1560
Qy 1775 CTTGATAAGAGAGAAAGCAGCATTCCTCCAAAGAGCTGCAGACCCGAGGCTTTCAGACAGC 1834
Db 1561 CTTGATAAGAGAGAAAGCAGCATTCCTCCAAAGAGCTGCAGACCCGAGGCTTTCAGACAGC 1620
Qy 1835 CAGAGCAAGCGATTGCTTCGGTTCAGAACCCAGCAGGTCGACCGCCAGAGGTCCTT 1894
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DEFINITION Sequence 115 from Patent WO0222660.
ACCESSION AX405700
VERSION AX405700.1 GI:21438839
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,P.,
Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 115 21-MAR-2002;
HYSEQ, INC. (US)
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AX278461
VERSION AX278461.1 GI:16605915
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 Duecker, K.
REFERENCE Identification of a dual specificity phosphatase: dusp-10
AUTHORS Patent: WO 017340-A 1 18-OCT-2001;
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QY 992 GACTTTATCCCGAGTCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGTGAGAA 1051
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QY 1112 TGTGTTCTAGTGCATCTGTTAGTGGGATCTCCGCTCCGCCACCATCGCTATCGCTAC 1171
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QY 1172 ATCATGAGAGAGTGGACATGCTTTTATAGTGAAGCTTACAGATTTGTGAAGAAAAAGA 1231
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QY 1412 CCACCTGTGCGGACTGTCTACCTCAGAGCGAGCAAGAAAGGCGCGCTGATCCGCG 1471
DB 1141 CCACCTGTGCGGACTGTCTACCTCAGAGCGAGCAAGAAAGGCGCGCTGATCCGCG 1200
QY 1472 AGCGTGCAGCGTGCAGCGCTGCGCTGTAGAGGACAGCGCGCTGGTACAG 1531
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QY 1832 AGCCAGAGCAAGGATTGCAATTCGTCAGAACAGCAGCAGTGGCAGCGCCAGCGTCC 1891

1561	Db	AGCCAGAGCAAGCCGATTGCAATTTCGGTTCAGAAACAGACGACAGTGGCACCGCCACAGGTCC	1620
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1621	Db	CTTTTATCTCACTGCATCGAAGTGGAGCGTGGAGGCAATTTACACACCAAGCTTCCTT	1680
1952	Qy	TTCCGCGCTTTCCACGCGACGACGACCTTCAGAAAGCTGCTGGCGCTGGCGCTTTAAGGGC	2011
1681	Db	TTCCGCGCTTTCCACGCGACGACGACCTTCAGAAAGCTGCTGGCGCTGGCGCTTTAAGGGC	1740
2012	Qy	TGGCACTCGGATATCTTTGGSCCCCCCAGACCTCTTACCCCTTCCCTGACCAAGCAGCTGGTAT	2071
1741	Db	TGGCACTCGGATATCTTTGGSCCCCCCAGACCTCTTACCCCTTCCCTGACCAAGCAGCTGGTAT	1800
2072	2y	TTTGCCACAGAGTCTCTACACTTCTTACTCTGCCTCAGCCATCTTACGAGGAGCGTGCAGT	2131
1801	Db	TTTGCCACAGAGTCTCTACACTTCTTACTCTGCCTCAGCCATCTTACGAGGAGCGTGCAGT	1860
2132	Qy	TACTCTGCTACAGCTGCAGCAGCTGCCACTTTGCGGAGACCAAGTCTATTCTGTGSCGC	2191
1861	Db	TACTCTGCTACAGCTGCAGCAGCTGCCACTTTGCGGAGACCAAGTCTATTCTGTGSCGC	1920
2192	2y	AGCGGCGAGAGCCAAAGTGACAGAGCTGACTCGCGCGAGCTGGCATGAGAGAGCGCC	2251
1921	Db	AGCGGCGAGAGCCAAAGTGACAGAGCTGACTCGCGCGAGCTGGCATGAGAGAGCGCC	1980
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1981	Db	TTTGAAGAGCAGTTTAAACGACAGACTGCCAAATGGBAATTTGGAGAGAGCATCATGTCA	2040
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2041	Db	GAGAACAGGTCAACGGGAAGAGCTGGGGGAAAGTGGCGAGTCAGTCTTAGCTTTTCGGGCAGC	2100
2372	2y	ATGGAAATCATTGAGTCTCCTGAGAGAGAAAGACACTTGTGACTTCTATAGACAAATTTTT	2431
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2732	2y	CGTTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTTCGGAGCCCTTCATAGTACACC	2791
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2792	2y	TTAGCGCTGAGACTGAGCCAGCTTTGGGGGTCAAGTATAGGTAGACCTGTGTAGGACAGAGC	2851
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2852	2y	CTAGTGGTAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCACAAAACCCACGCTCAC	2911
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Qy	3092	ACCAATTCAAAGTCTCTATGCACAAAATTCCTGGTGGCCCTAGATGGAGATAATTTTTTTTT	3151
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Qy	3212	CTGGCAACATCACGATTTAAGCTAAGGTTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGT	3271
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Search completed: February 27, 2004, 22:38:49
Job time : 12790 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run On: February 27, 2004, 18:38:58 ; Search time 1216 Seconds

(without alignments)
11640.622 Million cell updates/sec

Title: US-09-964-277-20

Perfect score: 3332

Sequence: 1 gagagaaggagaagataata.....ataaagatgaacttggtttc 3332

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002s.*

7: Geneseq2003as.*

8: Geneseq2003bs.*

9: Geneseq2003cs.*

10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3332	100.0	3332	6	ABK48378
2	3158	94.8	3496	6	ABK47596
3	3118.8	93.6	3766	6	ABK14474
4	3106.2	93.2	5450	6	ACC60559
5	3106.2	93.2	5450	6	ACC60572
6	2950	88.5	3544	5	RAA14639
7	2950	88.5	3544	6	ABK49402
8	2950	88.5	5145	5	ABV20833
9	2950	88.5	5145	5	ABV21080
10	2950	88.5	5145	5	ABV21080
11	2950	88.5	5145	5	ABV20978
12	2950	88.5	5145	5	ABV21092
13	2950	88.5	5145	5	ABV21312
14	2950	88.5	5145	5	ABV21316
15	2950	88.5	5145	5	ABV26826
16	2950	88.5	5145	5	ABV27131
17	2950	88.5	5145	5	ABV26923
18	2950	88.5	5145	5	ABV27135
19	2950	88.5	5145	5	ABV28657
20	2950	88.5	5145	5	ABV22827
21	2950	88.5	5145	5	ABV26934
22	2924.6	87.8	5111	6	ACC60521
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27	2390.8	71.8	2732	4	AAD09492	Aad09492 Human SGP
28	1762.4	52.9	2102	7	ADA53105	Ada53105 Human cod
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31	886.8	26.6	2558	9	ADB33596	ADB33596 Human CDN
32	595	17.9	787	4	AAI95265	Aai95265 Human neu
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38	417.2	12.5	425	5	ABV10726	Abv10726 Human pro
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42	409.2	12.3	478	8	ACC60561	Acc60561 Polynucle
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ALIGNMENTS

RESULT 1

ABK48378

ID ABK48378 standard; cDNA; 3332 BP.

XX

AC ABK48378;

XX

DT 02-JUL-2002 (first entry)

XX

DE cDNA encoding human DSP-16 alternative form protein.

XX

KW Human; dual-specificity phosphatase-3; DSP-16; autoimmune disease;
KW mitogen-activated protein kinase; MAP; Duchenne muscular dystrophy;
KW cancer; graft-versus-host disease; allergy; metabolic disease;

KW abnormal cell growth; abnormal cell proliferation; contact inhibition;

KW cell cycle abnormality; anchorage independent cell growth; apoptosis;

KW intercellular adhesion; DSP-16 modulator; chromosome 12p; gene; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS

FT 842..2395

FT /*tag= a

FT /product= "Human dual-specificity phosphatase-3 (DSP-16)

FT alternative form protein"

FT WO200226997-A2.

XX

PN 04-APR-2002.

XX

PF 25-SEP-2001; 2001WO-US030124.

XX

PR 26-SEP-2000; 2000US-0235487P.

XX

PA (CEPT-) CEPTVR INC.

XX

PI Luche RM, Wei B;

XX

XX WPI; 2002-315802/35.

DR P-PSDB; AAU79159.

XX

PT New DSP-16 polypeptide, useful for identifying modulators of its
PT activity, which can be used in the treatment of disorders such as
PT Duchenne muscular dystrophy, or cancer.

XX

PS Claim 56; Fig 3; 87pp; English.

XX


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RESULT 2
ABK47596
ID ABK47596 standard; cdna; 3496 BP.
XX
AC ABK47596;
XX
DT 02-JUL-2002 (first entry)
XX
DE cDNA encoding human dual-specificity phosphatase-3 (DSP-16) protein.
XX
KW Human; dual-specificity phosphatase-3; DSP-16; autoimmune disease;
KW mitogen-activated protein kinase; MAP; Duchenne muscular dystrophy;
KW cancer; graft-versus-host disease; allergy; metabolic disease;
KW abnormal cell growth; abnormal cell proliferation; contact inhibition;
KW cell cycle abnormality; anchorage independent cell growth; apoptosis;
KW intercellular adhesion; DSP-16 modulator; chromosome 12p; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 582..2559
FT /*tag= a
FT /product= "Human dual-specificity phosphatase-3 (DSP-16)
FT protein"
XX
XX WO200226997-A2.
XX
XX 04-APR-2002.
XX
XX 25-SEP-2001; 2001WO-US030124.
XX
XX 26-SEP-2000; 2000US-0235487P.
XX
XX (CEPT-) CEPTYR INC.
XX
XX Luche RM, Wei B;
XX WPI; 2002-315802/35.
XX P-PSDB; AAU79156.
XX
XX New DSP-16 polypeptide, useful for identifying modulators of its
XX activity, which can be used in the treatment of disorders such as
XX Duchenne muscular dystrophy, or cancer.
XX
```


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Db 2821 GAAATTAACATCTCTTCTTCTTAAAGAACAGTGTCTTTGGTGTGGAGGACAAATC 2880
QY 2717 CCCTACCAATTTTCCAGCTGTGTCTACTAAGAGATCTCAAAATATAGTCTTTTGCAGACC 2776

Db 2881 CCCTACCAATTTTCCAGCTGTGTCTACTAAGAGATCTCAAAATATTAGTCTTTTGTCCGAGCC 2940
QY 2777 CTTCCATAGTACACCTTTAGCGCTGAGACTGAGCCAGCTTGGGGGTTCAGGTAGGTAGACCC 2836
Db 2941 CTTCCATAGTACACCTTTAGCGCTGAGACTGAGCCAGCTTGGGGGTTCAGGTAGGTAGACCC 3000
QY 2837 TGTTAGGACAGAGCGCTAGTGGTAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCA 2896
Db 3001 TGTTAGGACAGAGCGCTAGTGGTAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCA 3060
QY 2897 CAAACCCACGCTCACCCTGACAGCCGAGGAGCACAGCATCACTCTCTGTGACGACCAAT 2956
Db 3061 CAAACCCACGCTCACCCTGACAGCCGAGGAGCACAGCATCACTCTCTGTGACGACCAAT 3120
QY 2957 AGGGCCCTTGCCAAAGTCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCGGG 3016
Db 3121 AGGGCCCTTGCCAAAGTCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCGGG 3180
QY 3017 CTTTGACCACTTACCATATCTGGTAGCCCATTTTCTAGGCATTTCTGAATAGGTAGGTAGCT 3076
Db 3181 CTTTGACCACTTACCATATCTGGTAGCCCATTTTCTAGGCATTTCTGAATAGGTAGGTAGCT 3240
QY 3077 AGTCACACTTTTCAGACCAATTCAAACTGTCTATGCAAAAAATTCGCGTGGGCTAGATG 3136
Db 3241 AGTCACACTTTTCAGACCAATTCAAACTGTCTATGCAAAAAATTCGCGTGGGCTAGATG 3300
QY 3137 GAGATAATTTTTTTTTTCTCTCAGCTTTATGAAGAGGGAACCTGTCTAGGATTCAGC 3196
Db 3301 GAGATAATTTTTTTTTTCTCTCAGCTTTATGAAGAGGGAACCTGTCTAGGATTCAGC 3360
QY 3197 TGAACCAACAGGAACTGGCAACATCAAGATTTAAGCTAAGGTGGAGGCTAACGAGTC 3256
Db 3361 TGAACCAACAGGAACTGGCAACATCAAGATTTAAGCTAAGGTGGAGGCTAACGAGTC 3420
QY 3257 TACCTCCCTCTTTGTAATCAAGAAATTTTAAATGGGATTTGCAATCTTTAATAA 3316
Db 3421 TACCTCCCTCTTTGTAATCAAGAAATTTTAAATGGGATTTGCAATCTTTAATAA 3480
QY 3317 AGATGAACCTTGGTTTC 3332
Db 3481 AGATGAACCTTGGTTTC 3496
RESULT 3
ABK14474
ID ABK14474 standard; cDNA; 3766 BP.
XX AC ABK14474;
XX DT 08-MAY-2002 (first entry)
XX Human protein phosphatase 7 (PP7) cDNA sequence.
DE Human; protein phosphatase 7; PP7; immune system disorder; AIDS;
KW acquired immunodeficiency syndrome; thymic hypoplasia; anaemia; asthma;
KW Crohn's disease; neurological disorder; epilepsy; Huntington's disease;
KW dementia; Parkinson's disease; developmental disorder; Down's syndrome;
KW cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma;
KW melanoma; myeloma sarcoma; gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
CDS 538..:2535
FT /*tag= a
FT /product= "Protein_phosphatase_7 (PP7)"
XX WO200210363-A2.
PN 07-FEB-2002.
XX PD 26-JUL-2001; 2001WO-US023716.
XX PF XX

XN		congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
OS		Homo sapiens.
XX		WO200257460-A2.
PX		25-JUL-2002.
PD		
PP		20-DEC-2001; 2001WO-US050459.
PR		20-DEC-2000; 2000US-0256868P.
PR		30-MAR-2001; 2001US-0280186P.
PN		01-MAY-2001; 2001US-0287735P.
PR		05-JUN-2001; 2001US-0295848P.
PR		25-JUN-2001; 2001US-0300465P.
XX		(BRIM) BRISTOL-MYERS SQUIBB CO.
FA		Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;
XX		Siemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;
PI		Krystek S, Mcatee P, Suchard S, Banas D;
XX		WPI; 2002-599721/64.
DR		P-PADB; ABR52381.
XX		
PT		Novel polynucleotides encoding human phosphatase polypeptides useful in
PT		the prevention or treatment of e.g. proliferative and cardiovascular
PT		disorders.
XX		Claim 1; Fig 13; 80pp; English.
PS		
XX		The invention relates to a novel isolated nucleic acid comprising a
CC		polynucleotide having a nucleotide sequence selected from 40
CC		polynucleotides fully defined in the specification. The polynucleotide of
CC		the invention has antiproliferative, hepatotropic, nephrotropic, or
CC		antiarthritic, anticypriatic, cardiant, and cytostatic activity. The
CC		polynucleotide may have a use in gene therapy. A polynucleotide or
CC		polypeptide of the invention is useful for preventing, treating or
CC		ameliorating a medical condition, e.g. a proliferative disorder. They are
CC		also useful for treating e.g. liver disease, renal failure, immunological
CC		disorders including arthritis and psoriasis, cardiovascular disorders
CC		such as congenital heart defects and congestive heart failure, and
CC		cancer. A method of the invention is useful for diagnosing a pathological
CC		condition or susceptibility to a condition in a subject. The present
CC		sequence is used in the exemplification of the invention
XX		
SQ		Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;
		Query Match 93.2%; Score 3106.2; DB 6; Length 5450;
		Best Local Similarity 95.1%; Pred. No. 0;
		Matches 3304; Conservative 0; Mismatches 3; Indels 166; Gaps 3
QY	25	GAAAGAAGAGGAGGAGGAGGAGCGACGGGACGGGAGCGGAGCGGAGCGGCCCTC
Db	1	GAAAGAAGAGCGAGGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGCCCTC
QY	85	TGGGTTCGGCGCGCGCGTCTGCATGTCGGGAGCGGAGGGGGGCCGAGGGGAGACGCC
Db	61	TGGGTTCGGCGCGCGCGTCTGCATGTCGGGAGCGGAGGGGGGCCGAGGGGAGACGCC
QY	145	GTGCAACTTTTCGTTTTCCCTCTGAGGGGAATTGGGAGGTTCGGCGCCCCCAAAGCTTTTAG
Db	121	GTGCAACTTTTCGTTTTCCCTCTGAGGGGAATTGGGAGGTTCGGCGCCCCCAAAGCTTTTAG
QY	205	TCCAGTGTAAGCTTTTGAGCGCGGGGAGCAAGGTTAAGAATGATGATATGCGTGGCT
Db	181	TCCAGTGTAAGCTTTTGAGCGCGGGGAGCAAGGTTAAGAATGATGATATGCGTGGCT
QY	265	GCTCCAAAGCATCTTTTGTGTGGAAUGGTTATTCCAGTCATCTCTTTATGATCAAAATG
Db	241	GCTCCAAAGCATCTTTTGTGTGGAAUGGTTATTCCAGTCATCTCTTTATGATCAAAATG
QY	325	TGAGGGGCTGCTTTTGTGGACGAGTCTTTTGCAAGAGCACATCAACGGGAAAGAGAAAGA

Db 1381 TCTCCAAACTTCAATTTCTGGGCCCACTCTGGACTATGAGAAGAGATTAGAACCAG 1440
QY 1301 ACTGGAGCATAGGGCCAAAGAGCAAACTCAAGCTGTGCACTCTGGAGAACCAAAATGAA 1360
Db 1441 ACTGGAGCATAGGGCCAAAGAGCAAACTCAAGCTGTGCACTCTGGAGAACCAAAATGAA 1500
QY 1361 CTTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAGCGAGAGCGCCCTCAGTCCACCCCTGT 1420
Db 1501 CTTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAGCGAGAGCGCCCTCAGTCCACCCCTGT 1560
QY 1421 GCGGACTCTGTCTCAGAGGACAGCAAGAAAGGCGGCTGCACTCCGCGAGCGTCCCC 1480
Db 1561 GCGGACTCTGTCTCAGAGGACAGCAAGAAAGGCGGCTGCACTCCGCGAGCGTCCCC 1620
QY 1481 ASCGTGCCAGCGTGCAGCGCTGCTGTAGAGGACAGCGCGCTGTACAGGCGCTCAGT 1540
Db 1621 AGCGTGCCAGCGTGCAGCGCTGCTGTGTAGAGGACAGCGCGCTGTACAGGCGCTCAGT 1680
QY 1541 GGGCTGCACCTCTCCGAGACAGCGTGGAGACAGCAATAAGCTCAAGCGTTCCTCTCT 1600
Db 1681 GGGCTGCACCTCTCCGAGACAGCGTGGAGACAGCAATAAGCTCAAGCGTTCCTCTCT 1740
QY 1601 CTGGATATCAATCAGTTTCATATTCAGCCAGCATGCGAGCATCTTACATGGCTTCC 1660
Db 1741 CTGGATATCAATCAGTTTCATATTCAGCCAGCATGCGAGCATCTTACATGGCTTCC 1800
QY 1661 TCATCAGAAGATGCTTTGGAACTACTACAAACCTTCCACTCTCTGGATGGAGCCAAACAG 1720
Db 1801 TCATCAGAAGATGCTTTGGAACTACTACAAACCTTCCACTCTCTGGATGGAGCCAAACAG 1860
QY 1721 CTATGCCAGTTCTCCCTGTTTCAGAACTATTCGAGAGCATCTCCGAAACAGCTCTGTAT 1780
Db 1861 CTATGCCAGTTCTCCCTGTTTCAGAACTATTCGAGAGCATCTCCGAAACAGCTCTGTAT 1920
QY 1781 AAGGAGGAAGCAGCATCCCAAGAGCTGCAGACCGCAGCGCTTCAGACAGCAGCAGC 1840
Db 1921 AAGGAGGAAGCAGCATCCCAAGAGCTGCAGACCGCAGCGCTTCAGACAGCAGCAGC 1980
QY 1841 AAGCATTTGCAATTCGGTCAGAAACAGCAGCAGTGGCACCGCCAGAGGTCCCTTTATCT 1900
Db 1981 AAGCATTTGCAATTCGGTCAGAAACAGCAGCAGTGGCACCGCCAGAGGTCCCTTTATCT 2040
QY 1901 CCACCTGCATCGAAGTGGAGCGTGGAGAGCAATTAACACACCGACTTCTCTTTTCGCGCTT 1960
Db 2041 CCACCTGCATCGAAGTGGAGCGTGGAGAGCAATTAACACACCGACTTCTCTTTTCGCGCTT 2100
QY 1961 TCCACCGACGACGACCTCACGAAGTCTGCTGGCTGGGCTTAAGGCTGGCACTCG 2020
Db 2101 TCCACCGACGACGACCTCACGAAGTCTGCTGGCTGGGCTTAAGGCTGGCACTCG 2160
QY 2021 GATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCGAGCCTGGTATTTCGACAC 2080
Db 2161 GATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCGAGCCTGGTATTTCGACAC 2220
QY 2081 GAGTCTCTCACACTTCTACTCTGCTCTCAGCCATCTACGGAGCGAGTGCAGTACTCTGCC 2140
Db 2221 GAGTCTCTCACACTTCTACTCTGCTCTCAGCCATCTACGGAGCGAGTGCAGTACTCTGCC 2280
QY 2141 TACAGTCTCAGCAGCTGCCCATCTTGGAGACCAAGTCTATTCTGTCGCGAGCGGCGAG 2200
Db 2281 TACAGTCTCAGCAGCTGCCCATCTTGGAGACCAAGTCTATTCTGTCGCGAGCGGCGAG 2340
QY 2201 AAGCCAAAGTGACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGAGCCCTTTGAAAG 2260
Db 2341 AAGCCAAAGTGACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGAGCCCTTTGAAAG 2400
QY 2261 CAGTTTAAACGAGAGCTGCCAATGGAAATTTGGAGAGCATCATGTTCAGAGAACAG 2320
Db 2401 CAGTTTAAACGAGAGCTGCCAATGGAAATTTGGAGAGCATCATGTTCAGAGAACAG 2460
QY 2321 TCACGGGAAGAGCTGGGAAAGTGGGAGTCAAGTCTAGCTTTTCGGGACGATGGAAATC 2380
Db 2461 TCACGGGAAGAGCTGGGAAAGTGGGAGTCAAGTCTAGCTTTTCGGGACGATGGAAATC 2520

RESULT 5

ACC60572

ID ACC60572 standard; cdna; 5450 BP.

XX ACC60572;

XX ACC60572;

DT 19-JUN-2003 (first entry)

QY 2381 ATTGAGGTCTCTCAGAGAAAGACACTTGTGACTTCTATAGACAA-TTTTTTTCTTG 2439
Db 2521 ATTGAGGTCTCTCAGAGAAAGACACTTGTGACTTCTATAGACAA-TTTTTTTCTTG 2580
QY 2440 TTCACAAAAAAATCCCTGTAAATCTGAATATATATATATATATATATATATATATATTTTG 2499
Db 2581 TTCACAAAAAAATCCCTGTAAATCTGAATATATATATATATATATATATATATATTTTG 2640
QY 2500 GAAATGGAGCTATGGTGTAAAGCAACAGGTGATCAACCCAGTTGTTACTCTCTTAAC 2559
Db 2641 GAAATGGAGCTATGGTGTAAAGCAACAGGTGATCAACCCAGTTGTTACTCTCTTAAC 2700
QY 2560 ATCTGCATTTTCAGAGATCAGTAATATCTTCTCAACAAAAATGGAAGGCGAGATGCTAG 2619
Db 2701 ATCTGCATTTTCAGAGATCAGTAATATCTTCTCTCAAAAAATGGAAGGCGAGATGCTAG 2760
QY 2620 AATCCCCCTTAGACGGAGGAAAAACCAATTTTATTCAGTGAATTTACATCTCTTGTTCCT 2679
Db 2761 AATCCCCCTTAGACGGAGGAAAAACCAATTTTATTCAGTGAATTTACATCTCTTGTTCCT 2820
QY 2680 AAAAAAGCAAGTGTCTTGTGTTGGAGGACAAATCCCTACATCCATTTCCAGCTGTGTGC 2739
Db 2821 AAAAAAGCAAGTGTCTTGTGTTGGAGGACAAATCCCTACATTTT-CACGTTGTGC 2879
QY 2740 TACTAAGAGATCTCAAAATATTTAGTCTTTGTCCGAGCCCTTCCATAGTACACCTTAGCGCT 2799
Db 2880 TACTAAGAGATCTCAAAATATTTAGTCTTTGTCCGAGCCCTTCCATAGTACACCTTAGCGCT 2939
QY 2800 GAGACTGAGCAGCTTGGGGTTCAGGTAGGTAGACCCCTGTTAGGACAGAGCTTAGTGT 2859
Db 2940 GAGACTGAGCAGCTTGGGGTTCAGGTAGGTAGACCCCTGTTAGGACAGAGCTTAGTGT 2999
QY 2860 AAATCCAAAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCACCTGCAGC 2919
Db 3000 AAATCCAAAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCACCTGCAGC 3059
QY 2920 CGAGGACACAGAGCATCACTCTGCTGGACGAGCAATTTAGGGGCTTTGCCAAGGCTTACCT 2979
Db 3060 CGAGGACACAGAGCATCACTCTGCTGGACGAGCAATTTAGGGGCTTTGCCAAGGCTTACCT 3119
QY 2980 TAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCGGGCTTTGACCACTACCATATCTGT 3039
Db 3120 TAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCGGGCTTTGACCACTACCATATCTGT 3179
QY 3040 AGCCCATTTTCTAGGCAATTTGAAATAGGTAGGTAGTCACTTTTCAGACCAATTC 3099
Db 3180 AGCCCATTTTCTAGGCAATTTGAAATAGGTAGGTAGTCACTTTTCAGACCAATTC 3239
QY 3100 AAATGCTATAGCAAAAAATCCGTTGGGCTTAGATGGAGATTAATTTTTTCTCTCA 3159
Db 3240 AAATGCTATAGCAAAAAATCCGTTGGGCTTAGATGGAGATTAATTTTTTCTCTCA 3299
QY 3160 GCTTTATGAAGAGAGGAAACTGCTTAGGATTCAGCTGAACCAACAGGAACTGCGAAC 3219
Db 3300 GCTTTATGAAGAGAGGAAACTGCTTAGGATTCAGCTGAACCAACAGGAACTGCGAAC 3359
QY 3220 ATCAAGATTTAAGTAAAGTTGGAGGCTTAAAGAGTCACTCTCTCTTTGTAATAACAA 3279
Db 3360 ATCAAGATTTAAGTAAAGTTGGAGGCTTAAAGAGTCACTCTCTCTTTGTAATAACAA 3419
QY 3280 GAATTTGTTTAAATGGGATTTCAATCCCTTTTAAATGAAGTGAACCTTGTTTC 3332
Db 3420 GAATTTGTTTAAATGGGATTTCAATCCCTTTTAAATGAAGTGAACCTTGTTTC 3472

QY 1181 AGGATGGACATGCTCTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTACTATA 1240
DB 1321 AGGATGGACATGCTCTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTACTATA 1380
QY 1241 TCTCCAAACTTCAATTTCTGGGCCAACTCTCGGACATATGAGAAAGATTTAAGAACAG 1300
DB 1381 TCTCCAAACTTCAATTTCTGGGCCAACTCTCGGACATATGAGAAAGATTTAAGAACAG 1440
QY 1301 ACTGGAGCATCAGGGCCAAAGGAACTCAAGCTGTGCACTCTGGAGAGCCAAATGAA 1360
DB 1441 ACTGGAGCATCAGGGCCAAAGGAACTCAAGCTGTGCACTCTGGAGAGCCAAATGAA 1500
QY 1361 CTTGTCCCTGCTGCTCTCAGAGGCTGACAGAAAGAGCAGCGCCCTCAGTCCACCCCTGT 1420
DB 1501 CTTGTCCCTGCTGCTCTCAGAGGCTGACAGAAAGAGCAGCGCCCTCAGTCCACCCCTGT 1560
QY 1421 GCCGACTCTGTCTCTCAGAGGCTGACAGAAAGAGCAGCGCCCTCAGTCCACCCCTGT 1480
DB 1561 GCCGACTCTGTCTCTCAGAGGCTGACAGAAAGAGCAGCGCCCTCAGTCCACCCCTGT 1620
QY 1481 AGCGTGCCAGCGTCCAGCGCTGCTGTAGAGCAGCGCCCTGCTACAGGCGCTCAGT 1540
DB 1621 AGCGTGCCAGCGTCCAGCGCTGCTGTAGAGCAGCGCCCTGCTACAGGCGCTCAGT 1680
QY 1541 GGGCTGCACCTGCTCCGACAGCAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCT 1600
DB 1681 GGGCTGCACCTGCTCCGACAGCAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCT 1740
QY 1601 CTGGATATCAATCAGTTTCATATTCAGCAGCATGAGGAGCATCTTACATGCTGCTCT 1660
DB 1741 CTGGATATCAATCAGTTTCATATTCAGCAGCATGAGGAGCATCTTACATGCTGCTCT 1800
QY 1661 TCATCAGAAAGTCTCTTGGAAATCTTACAAACCTTCCACTACTCTGGATGGAGCAACAAG 1720
DB 1801 TCATCAGAAAGTCTCTTGGAAATCTTACAAACCTTCCACTACTCTGGATGGAGCAACAAG 1860
QY 1721 CTATGCCATCTCTCCCTGTTTCAAGAACTATCGAGCAGACTCCCGAAACCAAGTCTGTAT 1780
DB 1861 CTATGCCATCTCTCCCTGTTTCAAGAACTATCGAGCAGACTCCCGAAACCAAGTCTGTAT 1920
QY 1781 AAGGAGGAAGCAGCATCCCAAGAGCTGCAGACCCGAGGCTTCAGACAGCCAGAGC 1840
DB 1921 AAGGAGGAAGCAGCATCCCAAGAGCTGCAGACCCGAGGCTTCAGACAGCCAGAGC 1980
QY 1841 AAGCAATTCGATTTGGTCAGAACAGCAGCAGTGGGCAACCGCCAGAGGTCCTTTTATCT 1900
DB 1981 AAGCAATTCGATTTGGTCAGAACAGCAGCAGTGGGCAACCGCCAGAGGTCCTTTTATCT 2040
QY 1901 CCACCTGCATCGAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTCTTTTCGGCCTT 1960
DB 2041 CCACCTGCATCGAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTCTTTTCGGCCTT 2100
QY 1961 TCCACAGCCAGCAGCAGCTTCAAGAGTCTGCTGGCCTGGGCTTAAGGCTGGCAGCTCG 2020
DB 2101 TCCACAGCCAGCAGCAGCTTCAAGAGTCTGCTGGCCTGGGCTTAAGGCTGGCAGCTCG 2160
QY 2021 GATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTATTTGGCCACA 2080
DB 2161 GATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTATTTGGCCACA 2220
QY 2081 GAGTCTCACAATCTTACTCTGCTCAGCCATCTACGGAGGAGTGCAGTTACTCTGCC 2140
DB 2221 GAGTCTCACAATCTTACTCTGCTCAGCCATCTACGGAGGAGTGCAGTTACTCTGCC 2280
QY 2141 TACAGCTCAGCAGCTGCCACCTTGGAGAGCAAGTCTATTTCTGCGCAGGCGGAC 2200
DB 2281 TACAGCTCAGCAGCTGCCACCTTGGAGAGCAAGTCTATTTCTGCGCAGGCGGAC 2340
QY 2201 AAGCCAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGCCCTTTGGAAG 2260
DB 2341 AAGCCAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGCCCTTTGGAAG 2400

QY 2261 CAGTTTAAACGACAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAGAGAACAGG 2320
DB 2401 CAGTTTAAACGACAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAGAGAACAGG 2460
QY 2321 TCACGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCTAGCTTTTTCGGGACAGCATGGAATC 2380
DB 2461 TCACGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCTAGCTTTTTCGGGACAGCATGGAATC 2520
QY 2381 ATTGAGGCTCTCTCAGAGAAAGACACTTGTGACTTCTATAGACAA-TTTTTTTTCTTG 2439
DB 2521 ATTGAGGCTCTCTCAGAGAAAGACACTTGTGACTTCTATAGACAA-TTTTTTTTCTTG 2580
QY 2440 TTCCAAAAAATTTCCCTGTAAATCTGAAATATATATATATATATATATATATATTTTG 2499
DB 2581 TTCCAAAAAATTTCCCTGTAAATCTGAAATATATATATATATATATATATATATTTTG 2640
QY 2500 GAAATGAGGCTATGTTGTAAAGCAACAGGTGATCAACCCAGTTTGTACTCTCTTAAC 2559
DB 2641 GAAATGAGGCTATGTTGTAAAGCAACAGGTGATCAACCCAGTTTGTACTCTCTTAAC 2700
QY 2560 ATCTGCATTTTTCAGAGATCAGCTAATCTCTCTCAACAAAAATGGAAGGCGCATGCTAG 2619
DB 2701 ATCTGCATTTTTCAGAGATCAGCTAATCTCTCTCAACAAAAATGGAAGGCGCATGCTAG 2760
QY 2620 AATCCCCCTAGACGGAGGAAACCAATTTTATTCAGTGAATTACACATCCTCTTGTCTT 2679
DB 2761 AATCCCCCTAGACGGAGGAAACCAATTTTATTCAGTGAATTACACATCCTCTTGTCTT 2820
QY 2680 AAAAAGCAAGTCTTGTGTTGGAGGACAAATCCCTCCTACCATTTTCCAGCTGTGTC 2739
DB 2821 AAAAAGCAAGTCTTGTGTTGGAGGACAAATCCCTCCTACCATTTT-CAGCTGTGTC 2879
QY 2740 TACTAAGAGATCTCAAAATATTAGTCTTGTCCGAGCCTTCCATAGTACACCTTAGCGCT 2799
DB 2880 TACTAAGAGATCTCAAAATATTAGTCTTGTCCGAGCCTTCCATAGTACACCTTAGCGCT 2939
QY 2800 GAGCTGAGCAGCTTGGGGTTCAGGTAGTACCCCTGTTAGGGAAGAGCCTTAGTGT 2859
DB 2940 GAGCTGAGCAGCTTGGGGTTCAGGTAGTACCCCTGTTAGGGAAGAGCCTTAGTGT 2999
QY 2860 AAATCCAAAGAAATGATCTTATCAAGCTGATTCACAAACCCAGCTCAGCTGACAGC 2919
DB 3000 AAATCCAAAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCAGCTGACAGC 3059
QY 2920 CGAGGGAACAGCAGCATCACTCTGCTGACAGGACCAATTAGGGGCTTTGCCAAGCTTACCT 2979
DB 3060 CGAGGGAACAGCAGCATCACTCTGCTGACAGGACCAATTAGGGGCTTTGCCAAGCTTACCT 3119
QY 2980 TAGAGCAAAACCCAGTACCTCAGACAGGAAGTGGGGCTTTGACCACTACCATATCTGCT 3039
DB 3120 TAGAGCAAAACCCAGTACCTCAGACAGGAAGTGGGGCTTTGACCACTACCATATCTGCT 3179
QY 3040 AGCCCAATTTTCTAGGCAATTTGATAGGTAGGTAGTCACTCTTTTTCAGACCAATTC 3099
DB 3180 AGCCCAATTTTCTAGGCAATTTGATAGGTAGGTAGTCACTCTTTTTCAGACCAATTC 3239
QY 3100 AAATGCTATGACAAAAATCCCGTGGGCTTAGATGGAGATAATTTTTTTTCTTCTCA 3159
DB 3240 AAATGCTATGACAAAAATCCCGTGGGCTTAGATGGAGATAATTTTTTTTCTTCTCA 3299
QY 3160 GCTTTATGAAGAGAGGGAACCTGTCTAGATTCAGCTGAACACACAGGAACCTGGCAAC 3219
DB 3300 GCTTTATGAAGAGAGGGAACCTGTCTAGATTCAGCTGAACACACAGGAACCTGGCAAC 3359
QY 3320 ATCAGATTTAAGCTAAGGTGGAGGCTTAAAGGCTACCTCCCTCTTTGTAATCAAA 3279
DB 3360 ATCAGATTTAAGCTAAGGTGGAGGCTTAAAGGCTACCTCCCTCTTTGTAATCAAA 3419
QY 3380 GAATTTGTTAAATGGATTTGTCATCTTTTAAATGAAGATGAACCTTGGTTTC 3332
DB 3420 GAATTTGTTAAATGGATTTGTCATCTTTTAAATGAAGATGAACCTTGGTTTC 3472

RESULT 6
AAS14639
ID AAS14639 standard; cDNA; 3544 BP.
XX AC
XX AC AAS14639;
XX DT
XX DT 18-DEC-2001 (first entry)
XX DE
XX DE Human cDNA encoding dual specificity phosphatase 21117.
XX KW
XX KW Human; ss; dual specificity phosphatase 21117; hepatotropic; cytostatic;
XX KW hematopoietic disorder; autoimmune disorder; diabetes mellitus;
XX KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
XX KW liver disorder; erythroid associated disorder; haemolytic anaemia;
XX KW cellular proliferative; differentiative disorder; leukaemia;
XX KW acute myeloid leukaemia; carcinoma; sarcoma; metastatic cancer.
XX OS
XX OS Homo sapiens.
XX FH
XX FH Key Location/Qualifiers
XX FT
XX FT CDS 589..2586
XX FT /*tag= a
XX FT /product= "Dual specificity phosphatase 21117"
XX FT
XX FN
XX FN W0200173059-A2.
XX PD
XX PD 04-OCT-2001.
XX PF
XX PF 23-MAR-2001; 2001WO-US009477.
XX PR
XX PR 24-MAR-2000; 2000US-0191858P.
XX PA
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI
XX PI Meyers RA;
XX XX
XX WPI; 2001-611635/70.
XX DR
XX DR P-PSDB; AAU09016.
XX PT
XX PT New human dual specificity polypeptides and nucleic acids for diagnosis
XX PT of disease and treatment of e.g. liver disorders.
XX PS
XX PS Claim 1; Fig 1; 143pp; English.
XX CC
XX CC The invention relates to two novel human dual specificity phosphatases
XX CC designated 21117 and 38692, the nucleic acids encoding them (including
XX CC fragments, allelic variants, their complements or nucleic acids that
XX CC hybridise to them) and antibodies raised against the proteins. The
XX CC antibody is useful for detecting the presence of the polypeptide, and the
XX CC nucleic acid fragments are useful for detecting the presence of the
XX CC nucleic acid, for diagnosing disease. Agents (e.g. the antibody and
XX CC antisense sequences) are useful for modulating the activity or expression
XX CC of the polypeptide/nucleic acid, useful for the treatment of e.g.
XX CC hematopoietic disorders, autoimmune disorders (e.g. diabetes mellitus,
XX CC rheumatoid arthritis, multiple sclerosis, Crohn's disease and many others
XX CC listed in the specification) liver disorders, erythroid associated
XX CC disorders (e.g. haemolytic anaemia) cellular proliferative or
XX CC differentiative disorders, leukaemias (e.g. acute myeloid leukaemia),
XX CC carcinomas, sarcomas, metastatic cancers. Agents modulating 21117 and
XX CC 38692 are also useful for modulating the proliferation, survival,
XX CC migration or differentiation of a 38692 or 21117-expressing cell. The
XX CC polypeptide and nucleic acids are useful for identifying modulating
XX CC agents. The present sequence encodes the dual specificity phosphatase
XX CC 21117
XX SQ
SQ Sequence 3544 BP; 1000 A; 840 C; 822 G; 882 T; 0 U; 0 Other;
Query Match 88.5%; Score 2950; DB 5; Length 3544;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;
QY 197 GCTTTCAGTCAAGTAAAGCTTTGGACGGGAGCAAGTAAGATGATGTAATG 256
|||||

Db 224 GCTTTCAGTCAAGTAAAGCTTTGGACGGGAGCAAGTAAGATGATGTAATG 283
QY 257 CGTGGCTGCTCCAAAGCATCTTTTGGTGTGGAATGGTTATTCCAGTCAATCTCTTTATGA 316
Db 284 CGTGGCTGCTCCAAAGCATCTTTTGGTGTGGAATGGTTATTCCAGTCAATCTCTTTATGA 343
QY 317 ATCAATGTGAGGGCTGCTTTGGACGGGAGTCTTTGCAAGAGCACATCAACGGGAAA 376
Db 344 ATCAATGTGAGGGCTGCTTTTGGACGGGAGTCTTTTGGACGGGAGTCTTTTGGACGGGAAA 403
QY 377 GAGAAGAGACATTACATTTGGAGGGCTCTTGTGAAATGGGTTTAACTCTCTCTTTTGGC 436
Db 404 GAGAAGAGACATTACATTTGGAGGGCTCTTGTGAAATGGGTTTAACTCTCTCTTTTGGC 463
QY 437 AGTACCACACCGCTGACCTCATACATTTTAGTACATGAGTGGCTGAGCCTTTGAGC 496
Db 464 AGTACCACACCGCTGACCTCATACATTTTAGTACATGAGTGGCTGAGCCTTTGAGC 523
QY 497 ACACACCATTTACATCATCTGTCGCAAAATTAAGAGAGGAGTGGGAAAAGAGCACTTATTG 556
Db 524 ACACACCATTTACATCATCTGTCGCAAAATTAAGAGAGGAGTGGGAAAAGAGCACTTATTG 583
QY 557 TTGTATGCCCCATGAGATGATTTGGAATCTCAAAATTTGTACTGAGAGGTTGTGCTCTGC 616
Db 584 TTGTATGCCCCATGAGATGATTTGGAATCTCAAAATTTGTACTGAGAGGTTGTGCTCTGC 643
QY 617 TGGAAAGTGGACGGGAAAAGTGTCTGCTAAATTTAGTACGCCGCCATTTGTGGAATACAAATA 676
Db 644 TGGAAAGTGGACGGGAAAAGTGTCTGCTAAATTTAGTACGCCGCCATTTGTGGAATACAAATA 703
QY 677 CATCCACATTTTGGAGCCATTAATATCAATCTGCTCCAAAGCTTATGAAGCAAGGTTGC 736
Db 704 CATCCACATTTTGGAGCCATTAATATCAATCTGCTCCAAAGCTTATGAAGCAAGGTTGC 763
QY 737 AACAGGACAAAGTGTAAATACAGAGCTATCCAGCATTCAGCGAAAACATAGGTTGACA 796
Db 764 AACAGGACAAAGTGTAAATACAGAGCTATCCAGCATTCAGCGAAAACATAGGTTGACA 823
QY 797 TTGATTGCACTCAGAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCCCTCTCTCT 856
Db 824 TTGATTGCACTCAGAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCCCTCTCTCT 883
QY 857 CTTTCAGACTTTTCTCACTGCTTCTGCTGAGTCTCTCGTTGTTTCCCTGGCTCTGTGAAGAAA 1003
Db 884 CTTTCAGACTTTTCTCACTGCTTCTGCTGAGTCTCTCGTTGTTTCCCTGGCTCTGTGAAGAAA 943
QY 917 ACCTGCTTGC----- 926
Db 944 ACCTGCTTGCAGGTGGGTTTGTGCTGAGTCTCTCGTTGTTTCCCTGGCTCTGTGAAGAAA 1003
QY 927 ----- 926
Db 1004 AATCCACTCTAGTCCCTACCTGCAATTTCTCAGCCCTGCTTACCTGTTGCCAACAATGGGC 1063
QY 927 -----AGGAGC 932
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Db 1124 TGATGACAGCAATGGGATTTGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCTG 1183
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QY 1113 GTGTTCTAGTGCACCTGTTAGTGGATCTCCGCTCCGCCACCATCGCTATCGCTTACCA 1172
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QY 1173 TCATGAGAGGATGGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC 1232
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Db 1724 CGCTCAGTGGGCTGCACCTGTCCGACAGAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1783
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QY 2073 TTGCCACAGAGTCTCAGACTTCTACTCTGCTCAGCCATCTACGGAGGAGTGGCCAGTT 2132
Db 2264 TTGCCACAGAGTCTCAGACTTCTACTCTGCTCAGCCATCTACGGAGGAGTGGCCAGTT 2323
QY 2133 ACTCTGCTACAGCTGACGAGCTGCCCTCCCTGCGAGACCAAGTCTATTCTGTGCGCA 2192
Db 2324 ACTCTGCTACAGCTGACGAGCTGCCCTCCCTGCGAGACCAAGTCTATTCTGTGCGCA 2383
QY 2193 GCGCGCAGAACCAAGTACAGACTGACTCGCGGCGAGCTGGCATGAGAGAGCCCT 2252
Db 2384 GCGCGCAGAACCAAGTACAGACTGACTCGCGGCGGAGCTGGCATGAGAGAGCCCT 2443

QY 2253 TTGAAAGCAGCTTTAAAGCGAGAAAGCTGCCAAATGGAATTTGGAGAGAGCATATGTGAG 2312
Db 2444 TTGAAAGCAGCTTTAAAGCGAGAAAGCTGCCAAATGGAATTTGGAGAGAGCATATGTGAG 2503
QY 2313 AGAACAGCTCAGCGGAGAGCTGGGAAAGTGGGCACTGAGTCTAGCTTTTCGGGAGCA 2372
Db 2504 AGAACAGCTCAGCGGAGAGCTGGGAAAGTGGGCACTGAGTCTAGCTTTTCGGGAGCA 2563
QY 2373 TGGAAATCAITTAGAGTCTCTGAGAGAAAGACACTTTGTGACTCTTATAGACAATTTTT 2432
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QY 2433 TTTCTGTGTTCAAAAAAATTTCCCTGTAAATCTGAAATATATATATATATATATATAT 2492
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QY 2493 ATTTTGGAAATGAGCTATGTGTAAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2552
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QY 2553 TCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGGCGAG 2612
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Db 2804 ATGCTAGAAATCCCCCTTAGACGGAGGAAACCAATTTTATTCAGTGAATTACACATCCTCT 2863
QY 2673 TGTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGGACAAAAATCCCTTACCATTTTCCAC 2732
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QY 2733 GTTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGAGCCCTTCCATAGTACACCT 2792
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Db 2983 TAGCGCTGAGACTGAGCCAGCTTGGGGGTGAGTGTAGAGCCCTGTTAGGGACAGAGCC 3042
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QY 2973 TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCCGGGCTTTGACCACTACCAT 3032
Db 3163 TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCCGGGCTTTGACCACTACCAT 3222
QY 3033 ATCTGTAGGCCCAATTTTCTAGGCAATTTGAAATAGGTAGGTAGTGTAGTGTAGTGTAGT 3092
Db 3223 ATCTGTAGGCCCAATTTTCTAGGCAATTTGAAATAGGTAGGTAGTGTAGTGTAGTGTAGT 3282
QY 3093 CCAATTCAACTGTCTATGCAAAAAATTTCCGTGGGCTGTAGATGAGAGATAATTTTTTTTT 3152
Db 3283 CCAATTCAACTGTCTATGCAAAAAATTTCCGTGGGCTGTAGATGAGAGATAATTTTTTTTT 3342
QY 3153 CTTCTCAGCTTTATGAAGAGAGGAAACCTGCTAGGATTCAGCTGAACCAACAGGAAAC 3212
Db 3343 CTTCTCAGCTTTATGAAGAGAGGAAACCTGCTAGGATTCAGCTGAACCAACAGGAAAC 3402
QY 3213 TGGCAACATCAGATTTAAGCTAAGGTGGGAGGTAAAGGTCTACCTCCCTCTTTGTA 3272
Db 3403 TGGCAACATCAGATTTAAGCTAAGGTGGGAGGTAAAGGTCTACCTCCCTCTTTGTA 3462
QY 3273 AATCAAGAAATCTGTTTAAATGGATGGATTCCTTTAAATAAAGATGAATCTGGTTTC 3332
Db 3463 AATCAAGAAATCTGTTTAAATGGATGGATTCCTTTAAATAAAGATGAATCTGGTTTC 3522

RESULT 7
 ID ABK49402
 XX ABK49402 standard; CDNA; 3544 BP.
 AC ABK49402;
 XX 02-JUL-2002 (first entry)
 XX cDNA encoding human dual specificity phosphatase 21117 protein.
 DE Human; dual specificity phosphatase 21117; erythroid-related disorder;
 XX haematopoietic-related disorder; leukaemia; autoimmune disease; anaemia;
 KW erythrocytosis; liver-related disorder; cancer; gene; ss.
 XX Homo sapiens.
 OS
 XX
 PH Key Location/Qualifiers
 FT CDS 589..2586
 FT /tag= a
 FT /product= "Human dual specificity phosphatase 21117"
 FT /note= "Specifically claimed in claim 2"
 XX
 XX US2002034807-A1.
 XX
 XX 21-MAR-2002.
 XX
 XX 23-MAR-2001; 2001US-00816494.
 XX
 XX 24-MAR-2000; 2000US-0191858P.
 XX
 XX (MEYE/) MEYERS R A.
 XX
 XX Meyers RA;
 PT WPI; 2002-351088/38.
 DR P-PSDB; AAU79929.
 XX
 XX New nucleic acids, designated 38692 and 21117, encoding dual specificity
 PT phosphatases for treating cell proliferation and differentiation
 PT disorders including hematopoietic and erythroid-related disorders and
 PT cancers.
 XX
 XX Claim 2; Fig 1; 76pp; English.
 XX
 XX The present invention relates to new nucleic acids designated 38692 and
 CC 21117 encoding dual specificity phosphatase family members. The nucleic
 CC acid, polypeptide encoded by it, and antibody specific for the
 CC polypeptide may be used to diagnose and treat haematopoietic-related
 CC disorders such as leukaemias and autoimmune diseases, erythroid-related
 CC disorders such as anaemias and erythrocytosis, liver-related disorders,
 CC and cancers, particularly of the breast, colon, adipose, prostate and
 CC lung. The present nucleic acid sequence encodes the human dual
 CC specificity phosphatase 21117 protein of the invention, as described
 CC above
 XX
 SQ Sequence 3544 BP; 1000 A; 840 C; 822 G; 882 T; 0 U; 0 Other;
 Query Match 88.5%; Score 2950; DB 6; Length 3544;
 Best Local Similarity 95.0%; Pred. No. 0;
 Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;
 197 GCTTTTCAGTCCAGTGTAAAGCTGTTGGAGCGGGGAGCAAAAGTAAAGATGATGTAATG 256
 224 GCTTTTCAGTCCAGTGTAAAGCTGTTGGAGCGGGGAGCAAAAGTAAAGATGATGTAATG 283
 257 CGTGGCTGCTCCAAAGCATCTTTGTTGGAGCGAGTCTTTGGAAGTATTCAGTCACTCTTTATGA 316
 284 CGTGGCTGCTCCAAAGCATCTTTGTTGGAGCGAGTCTTTGGAAGTATTCAGTCACTCTTTATGA 343
 317 ATCAAAATGTGAGGGGTGCTTTGTTGGAGCGAGTCTTTGGAAGTATTCAGTCACTCTTTATGA 376
 344 ATCAAAATGTGAGGGGTGCTTTGTTGGAGCGAGTCTTTGGAAGTATTCAGTCACTCTTTATGA 403

377 GAGAAAGAGACATTCACCTGGAGGCTCTTCTGCTGAATGGTCTTAACCTCCCTTTTGGC 436
 404 GAGAAAGAGACATTCACCTGGAGGCTCTTCTGCTGAATGGTCTTAACCTCCCTTTTGGC 463
 437 AGTCACCAACAGCTGACCTCATACATTTTGTAGTCAATGGAGTGGCTGAGCCTTTGAGC 496
 464 AGTCACCAACAGCTGACCTCATACATTTTGTAGTCAATGGAGTGGCTGAGCCTTTGAGC 523
 497 ACACACACATTCATCATCGTGGCAATTAAGAGAGGAGTGGGAAAGAGGAGCTTATTG 556
 524 ACACACACATTCATCATCGTGGCAATTAAGAGAGGAGTGGGAAAGAGGAGCTTATTG 583
 557 TTGTGATGCGCCCATGAGATGATTGGAATCAAAATGTTTACTGAGAGGTTGGTGGCTCTGC 616
 584 TTGTGATGCGCCCATGAGATGATTGGAATCAAAATGTTTACTGAGAGGTTGGTGGCTCTGC 643
 617 TGGAAAGTGGAAACGGAATAAGTGTCTGCTTAATGATAGCGGCCCATTTGTGGAATACAAATA 676
 644 TGGAAAGTGGAAACGGAATAAGTGTCTGCTTAATGATAGCGGCCCATTTGTGGAATACAAATA 703
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 704 CATCCACATTTTGGAGGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGC 763
 737 AACAGGACAAAGTGTAAATTAAGAGCTCATTCAGCATTCAGCGAAACATAAGGTTGACA 796
 764 AACAGGACAAAGTGTAAATTAAGAGCTCATTCAGCATTCAGCGAAACATAAGGTTGACA 823
 797 TTGATTGCAAGTCAGAAAGTGTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCT 856
 824 TTGATTGCAAGTCAGAAAGTGTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCT 883
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 884 CTTGAGACTGTTTCTCAGTCTACTCTGTTGGTAAACTGGAGAGAGGTTCAACTCTCTTTC 943
 917 ACCTGCTTGC----- 926
 944 ACCTGCTTGCAGGTGGTGTGCTGAGTCTCTGTTGTTTCCCTGGCCTCTGTGAAGGAA 1003
 927 ----- 926
 1004 AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGTCTTACCTGTTGCCAACATTTGGGC 1063
 927 -----AGAGC 932
 1064 CAACCCGAATTTTCCCAATCTTTATCTGTGCTGCCAGAGATGTCTCTCAACAGAGC 1123
 933 TGATGAGCAGAAATGGGATTTGGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCTG 992
 1124 TGATGAGCAGAAATGGGATTTGGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCTG 1183
 993 ACTTTATCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTTGTGAGAAAA 1052
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 1244 TTTTCCGCTGTTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCCTCCAATGGAT 1303
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 1173 TCATGAAGGAGTGGACATGCTTTTGTAGTGAAGCTTACAGTTTGTGAAGAAAAAGAC 1232
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 1293 AGAACGAGCTGGAGCATCAGGGCCAAAGCAAACTCAAGCTGCTGCACCTGGAGAGC 1352

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Qy 1353 CAAATGAACCTGTCCTGCTGTCTCAGAGGCTGGACAGAAAGCAGAGAGCGCCCTCAGTC 1412
Db 1544 CAAATGAACCTGTCCTGCTGTCTCAGAGGCTGGACAGAAAGCAGAGAGCGCCCTCAGTC 1603
Qy 1413 CACCTGTGCGCACTGTCTACTCTCAGAGGCGAGCAGGACAAAGGCGCGTGCATCCCGCA 1472
Db 1604 CACCTGTGCGCACTGTCTACTCTCAGAGGCGAGCAGGACAAAGGCGCGTGCATCCCGCA 1663
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Db 1724 CGCTCAGTGGGCTGCACCTGTCCGACAGCAGGCTGGAAGACAGCANAAAGCTCAAGCGTT 1783
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Qy 1773 GTCCTGATTAAGAGAGAGCGAGCTCCCGAGAGAGCTGCAGAGCGCGCAGGCTTCAGACA 1832
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Db 2024 GCCAGAGCAGAGATGCGATTCGGTTCAGAAACAGCAGCAGTGGCAGCGCCAGAGGTCCC 2083
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Db 2264 TTGCCACAGAGTCTCAGCTTCTACTTCTGCTCAGCAGCTATCAGGAGGAGTGCAGTT 2323
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Db 2384 GCGGCGAGAGCCAGTGAAGAGCTGACTTCGCGGCGGAGCTGGCATGAAGAGAGCCCT 2443
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Qy 3033 ATCTGTAGCCCAATTTCTTAGGCAATTTGTAATAGTGTAGTGTAGTGTAGTGTAGTGTAG 3092
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Db 3403 TGGCAACATCAGCATTTAAGCTAAGGTTCGGAGGCTTAACAGTCTACCTCCCTCTTTGTA 3462
Qy 3273 AATCAAGAAATGTTTAAATGGGATTTGTCATCTTTAAATATAAGATGAATCTTGGTTTC 3332
Db 3463 AATCAAGAAATGTTTAAATGGGATTTGTCATCTTTAAATATAAGATGAATCTTGGTTTC 3522

RESULT 8
ABV20833
ID ABV20833 standard; cDNA; 5145 BP.
XX
AC ABV20833;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 20824.
XX

Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; pharmacogenomic marker; gene; ss.

Homo sapiens.

WO200160860-A2.

23-AUG-2001.

20-FEB-2001: 2001WO-US005171.

17-FEB-2000: 2000US-0183319P

I6-MAR-2000; 2000US-0189862P.
 2E-MAY-2000; 2000US-0307454P

09-JUN-2000; 2000US-0211314P.

13-DEC-2000; 2000US-0255281P.

(MILL-) MILLENNIUM PREDICTIVE

Schlegel R, Endege WO, Monna

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule

prostate cells and correlating with
for detecting presence of prostate c

Claim 1: Page 3479. 11750nn. English

1. Constitution
 2. Executive
 3. Legislative
 4. Judicial
 5. Local Government
 6. Public Administration
 7. Public Finance
 8. Public Health
 9. Public Welfare
 10. Public Works
 11. Public Safety
 12. Public Education
 13. Public Housing
 14. Public Transportation
 15. Public Utilities
 16. Public Services
 17. Public Information
 18. Public Relations
 19. Public Opinion
 20. Public Policy
 21. Public Law
 22. Public Order
 23. Public Security
 24. Public Peace
 25. Public Justice
 26. Public Liberty
 27. Public Equality
 28. Public Fraternity
 29. Public Solidarity
 30. Public Responsibility
 31. Public Accountability
 32. Public Transparency
 33. Public Integrity
 34. Public Honesty
 35. Public Trust
 36. Public Respect
 37. Public Dignity
 38. Public Honor
 39. Public Reputation
 40. Public Image
 41. Public Brand
 42. Public Identity
 43. Public Character
 44. Public Virtue
 45. Public Wisdom
 46. Public Courage
 47. Public Strength
 48. Public Power
 49. Public Authority
 50. Public Influence
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 52. Public Fame
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 134. Public Reputation
 135. Public Image
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 155. Public Brand
 156. Public Identity
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 158. Public Virtue
 159. Public Wisdom
 160. Public Courage
 161. Public Strength
 162. Public Power
 163. Public Authority
 164. Public Influence
 165. Public Prestige
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 167. Public Glory
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 169. Public Respect
 170. Public Dignity
 171. Public Honor
 172. Public Reputation
 173. Public Image
 174. Public Brand
 175. Public Identity
 176. Public Character
 177. Public Virtue
 178. Public Wisdom
 179. Public Courage
 180. Public Strength
 181. Public Power
 182. Public Authority
 183. Public Influence
 184. Public Prestige
 185. Public Fame
 186. Public Glory
 187. Public Honor
 188. Public Respect
 189. Public Dignity
 190. Public Honor
 191. Public Reputation
 192. Public Image
 193. Public Brand
 194. Public Identity
 195. Public Character
 196. Public Virtue
 197. Public Wisdom
 198. Public Courage
 199. Public Strength
 200. Public Power
 201. Public Authority
 202. Public Influence
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 205. Public Glory
 206. Public Honor
 207. Public Respect
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 209. Public Honor
 210. Public Reputation
 211. Public Image
 212. Public Brand
 213. Public Identity
 214. Public Character
 215. Public Virtue
 216. Public Wisdom
 217. Public Courage
 218. Public Strength
 219. Public Power
 220. Public Authority
 221. Public Influence
 222. Public Prestige
 223. Public Fame
 224. Public Glory
 225. Public Honor
 226. Public Respect
 227. Public Dignity
 228. Public Honor
 229. Public Reputation
 230. Public Image
 231. Public Brand
 232. Public Identity
 233. Public Character
 234. Public Virtue
 235. Public Wisdom
 236. Public Courage
 237. Public Strength
 238. Public Power
 239. Public Authority
 240. Public Influence
 241. Public Prestige
 242. Public Fame
 243. Public Glory
 244. Public Honor
 245.

a nucleotide sequence given in Tables 1-5 (ABV000.10-ABV022.1) or the specification of its complement. (f) is useful for (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or incidence of prostate cancer in a patient. (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 5145 BP: 1408 A: 1135 C: 1253 G: 1346 T: 0 U: 3 Other:

```
Query Match      88.5%; Score 2950; DB 5; Length 5145;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2
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197 GCTTTCAGTCCAGTGTAAGCTGTTGGAGCGCGGAGCAAAGGTAAGAAATGATGTAATG 256

224 GCTTTCAGTCCAGTGTAAGCTGTTGGAGCGCGGAGCAAGGTAAGAAATGATGTAATG 283

257 CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAAATGGTTATTCAGTCATCTCTTTATGA 316

384 CCCTCCGCGCCTCCAAAGCCATCTTTTCTGTGGAAATGGTTATTCCAGTCATGCCTTTTATGA 343

376

[illegible][illegible]

404 AGTCAACCCAGGCCCTGACCCTCATACACTTTTAATACAACTAATGATGGCCTGTGCGCTTTCGCTT

[illegible]

PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JB;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 3481; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV0010-ABV6213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
XX
XX Query Match 88.5%; Score 2950; DB 5; Length 5145;
XX Best Local Similarity 95.0%; Pred. No. 0;
XX Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;
XX
XX 197 GCTTTCAGTCCAGTGAAGCTTTGGAGCGGGAGCAAGGTAAGAAATGATGTAATG 256
XX 224 GCTTTTCAGTCCAGTGAAGCTTTGGAGCGGGAGCAAGGTAAGAAATGATGTAATG 283
XX 257 CGCTGGCTGCTCCAAAGCATCTTTTGTGGAAATGGTTATTCAGTCACTCTTTTATGA 316
XX 284 CGCTGGCTGCTCCAAAGCATCTTTTGTGGAAATGGTTATTCAGTCACTCTTTTATGA 343
XX 317 ATCAATATGAGGGGTGCTTTGTGAGCGGAGTCTTTGCAAGAGACATCAACGGGAAA 376
XX 344 ATCAATATGAGGGGTGCTTTGTGAGCGGAGTCTTTTGAAGAGACATCAACGGGAAA 403
XX 377 GAGAAAGAGACATCACTTGGAGGGCTCTTGTGAAATGGTTTAACTCTCTTTTGGCC 436
XX 404 GAGAAAGAGACATCACTTGGAGGGCTCTTGTGAAATGGTTTAACTCTCTTTTGGCC 463
XX 437 AGTCACACAGCGCTGACCTCATACATCTTTTGTAGTCAATGGAGTGGCTTGTGAGC 496
XX 464 AGTCACACAGCGCTGACCTCATACATCTTTTGTAGTCAATGGAGTGGCTTGTGAGC 523
XX 497 ACACCACCATATCATCTGTCGAATTAAGAGAGGAGTGGGAAAGAGAGACTTATTG 556
XX 524 ACACCACCATATCATCTGTCGAATTAAGAGAGGAGTGGGAAAGAGAGACTTATTG 583
XX 557 TTGTTCATGGCCCATGAGATGATTTGGAACCTCAATTTTACTGAGAGGTTTGTGGCTTGC 616
XX 584 TTGTTCATGGCCCATGAGATGATTTGGAACCTCAATTTTACTGAGAGGTTTGTGGCTTGC 643
XX 617 TGGAAATGGAACGGAAAAGTCTGCTTAATGATAGCCGGCCATTTGTGGAAATCAATA 676
XX 644 TGGAAATGGAACGGAAAAGTCTGCTTAATGATAGCCGGCCATTTGTGGAAATCAATA 703
XX 677 CATCCCACTTTTGGAAAGCATTAATCAACTGTCTCAAGCTTATGAAGCGAAGGTTGC 736
XX 704 CATCCCACTTTTGGAAAGCATTAATCAACTGTCTCAAGCTTATGAAGCGAAGGTTGC 763
QY 737 AACAGGACAAAGTGTTAATTAACAGAGCTCATCCAGCATTTCCAGCGAAAACATAAGTTGACA 796
DB 764 AACAGGACAAAGTGTTAATTAACAGAGCTCATCCAGCATTTCCAGCGAAAACATAAGTTGACA 823
QY 797 TTGATGAGAGTCAGAAAGTGTGATTTACGATCAAGCTCCCAAGATGTTGGCTCTCTCT 856
DB 824 TTGATGAGAGTCAGAAAGTGTGATTTACGATCAAGCTCCCAAGATGTTGGCTCTCTCT 883
QY 857 CTTTCAGACTGTTTCTCACTGATCTTCTGGGTAACCTGGAGAGAGCTTCAACTCTCTTC 916
DB 884 CTTTCAGACTGTTTCTCACTGATCTTCTGGGTAACCTGGAGAGAGCTTCAACTCTCTTC 943
QY 917 ACTCTCTTGC----- 926
DB 944 ACTCTCTTGCAGGTGGTGTGCTGAGTTCTCTCGTTGTTTCCCTGGCTCTGTGAAGAA 1003
QY 927 ----- 926
DB 1004 AATCCACTTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACCTGTGGCAACATTGGGC 1063
QY 927 -----AGAGC 932
DB 1064 CAACCGAATTTCTCCCAATCTTTTATCTTGCTGCGAGAGATGCTCTCAACAAAGAGC 1123
QY 933 TGATGAGCAGATGGGATTTGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCTG 992
DB 1124 TGATGAGCAGATGGGATTTGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCTG 1183
QY 993 ACTTTATCTCCCGAGTCTCATTTCTCTGCTGCTGTGAATGACAGCTTTTGTGAGAAA 1052
DB 1184 ACTTTATCTCCCGAGTCTCATTTCTGCTGCTGTGAATGACAGCTTTTGTGAGAAA 1243
QY 1053 TTTTGCCTGGTTGGACAAATCAGTAGATTTTCATGAGAAAGCAAAAGCTTCCATCGAT 1112
DB 1244 TTTTGCCTGGTTGGACAAATCAGTAGATTTTCATGAGAAAGCAAAAGCTTCCATCGAT 1303
QY 1113 GTGTTCTAGTGACATGTTTAGCTGGGATCTCCCGCTCGCCACCATCGCTATCGCTACA 1172
DB 1304 GTGTTCTAGTGACATGTTTAGCTGGGATCTCCCGCTCGCCACCATCGCTATCGCTACA 1363
QY 1173 TCATGAAGAGATGACATGTTTGTAGATGAGCTTACAGATTTGTGAAGAAAAGAC 1232
DB 1364 TCATGAAGAGATGACATGTTTGTAGATGAGCTTACAGATTTGTGAAGAAAAGAC 1423
QY 1233 CTACTATATCTCCAACTTCAATTTCTGGGCAACTCTCTGACTATGAGAAAGATTA 1292
DB 1424 CTACTATATCTCCAACTTCAATTTCTGGGCAACTCTCTGACTATGAGAAAGATTA 1483
QY 1293 AGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTCTGCACTGGAGAGC 1352
DB 1484 AGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTCTGCACTGGAGAGC 1543
QY 1353 CAAATGAACCTGCTCCTGCTGCTCAGAGGGTGGACAGAAAGCGAGACGCCCTCAGTC 1412
DB 1544 CAAATGAACCTGCTCCTGCTGCTCAGAGGGTGGACAGAAAGCGAGACGCCCTCAGTC 1603
QY 1413 CACCTGTGCTCCGACTCTGCTACTCAGAGGCGAGGAGCAAAAGGCCGCTGCATCCGCCA 1472
DB 1604 CACCTGTGCTCCGACTCTGCTACTCAGAGGCGAGGAGCAAAAGGCCGCTGCATCCGCCA 1663
QY 1473 GGTGCGCCAGGTGCGCAGCTGCGCTGCTGTTAGAGCAGCGCCGCTGTGACAGG 1532
DB 1664 GGTGCGCCAGGTGCGCAGCTGCGCTGCTGTTAGAGCAGCGCCGCTGTGACAGG 1723
QY 1533 CGCTCAGTGGGTGCACTGCTGCTGCTGCGCAGACAGCTGGAGAGCAGCAATAAGCTCAAGGTT 1592
DB 1724 CGCTCAGTGGGTGCACTGCTGCTGCTGCGCAGACAGCTGGAGAGCAGCAATAAGCTCAAGGTT 1783
QY 1593 CTTTCTCTCGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATG 1652
DB 1784 CTTTCTCTCGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATG 1843
QY 1653 GCTTCTCTCTCATCAGAGATGCTTTGGAAATCACTACAAACCTTCCACTACTCTGGATGGGA 1712

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1: Page 5388-5389; 11750pp: English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacoeconomic marker.

Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

```
Query Match      88.5%; Score 2950; DB 5; Length 5145;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;
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197	QY	GC	TTTCAGTC	CAAGTGTAAAGCTGTTGGAGCGCGGAGCAAGGTAAGAATGATGTAATG	256
224	DB	GC	TTTCAGTC	CAAGTGTAAAGCTGTTGGAGCGCGGAGCAAGGTAAGAATGATGTAATG	283
257	QY	GC	TGGCTGCT	CCAAAGCATCTTTTGTGTGGAAATGTTATTCAGTCATCTCTTTATGA	316
284	DB	GC	TGGCTGCT	CCAAAGCATCTTTTGTGTGGAAATGTTATTCAGTCATCTCTTTATGA	343
317	QY	AT	CAAAATGT	GAGGGCTGCTTTGTGGACGAGTCCCTTTCAGAGCACATCAACGGGAAA	376
344	DB	AT	CAAAATGT	GAGGGCTGCTTTGTGGACGAGTCCCTTTCAGAGCACATCAACGGGAAA	403
377	QY	GGA	GAAGAGACA	TTCACCTTGGAGGGCTCTTGTGGAATGGGTTTAACTCTCCTTTTGCC	436
404	DB	GGA	GAAGAGACA	TTCACCTTGGAGGGCTCTTGTGGAATGGGTTTAACTCTCCTTTTGCC	463
437	QY	AGT	CACCA	CCAGCTGACCTCATACATTTTGTAGTACAAATGGAGTGGCTGAGCCTTTGAGC	496
464	DB	AGT	CACCA	CCAGCTGACCTCATACATTTTGTAGTACAAATGGAGTGGCTGAGCCTTTGAGC	523
497	QY	AC	ACCACCA	TTCATCATCTGGTGGCAAAATTAAGNAGGAGTGGGAAAAGAGGACCTTATG	556
524	DB	AC	ACCACCA	TTCATCATCTGGTGGCAAAATTAAGNAGGAGTGGGAAAAGAGGACCTTATG	583
557	QY	TTG	TCTCAT	GGCCCATGAGATGATTCGAACTCAAATTTGTTACTGAGAGGTTTGGTGCTCTGC	616
584	DB	TTG	TCTCAT	GGCCCATGAGATGATTCGAACTCAAATTTGTTACTGAGAGGTTTGGTGCTCTGC	643
617	QY	TG	AAAGTGG	AAACGGAAAGTGCTGCTAATTTGATAGCGGCCCATTTGTGGAAATACAATA	676
644	DB	TG	AAAGTGG	AAACGGAAAGTGCTGCTAATTTGATAGCGGCCCATTTGTGGAAATACAATA	703
677	QY	CA	TCCCA	CAATTTTGGAGCCATTAATTAACATGTCTCCAAGCTTATGAAGCGAAGTTGC	736
704	DB	CA	TCCCA	CAATTTTGGAGCCATTAATTAACATGTCTCCAAGCTTATGAAGCGAAGTTGC	763
737	QY	AA	CAGCA	CAAAAGTGTAAATTAACAGAGTCTCATCAGCAATTCAGCGAAACATAAAGTTGACA	796
764	DB	AA	CAGCA	CAAAAGTGTGTAAATTAACAGAGTCTCATCAGCAATTCAGCGAAACATAAAGTTGACA	823
797	QY	TTG	ATTG	CAGTCCAGAAGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCT	856
824	DB	TTG	ATTG	CAGTCCAGAAGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCT	883
857	QY	CTT	CAGCTG	TTTTCTCACTGACTCTCTCGGGTAAACTGGAGAGAGCTTCAACTCTGTTTC	916
884	DB	CTT	CAGCTG	TTTTCTCACTGACTCTCTCGGGTAAACTGGAGAGAGCTTCAACTCTGTTTC	943

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Query Match		88.5%; Score 2950; DB 5; Length 5145;
Best Local Similarity		95.0%; Pred. No. 0;
Matches 3135; Conservative		0; Mismatches 0; Indels 165; Gaps 2;
QY	197	GCCTTCAGTCAGGTAAAGCTCTCGAGCGGGAGCAAGTAAGAAATGATGTAATG 256
DB	224	GCCTTCAGTCAGGTAAAGCTCTCGAGCGGGAGCAAGTAAGAAATGATGTAATG 283
QY	257	CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATCCAGTCATCTTTATGA 316
DB	284	CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATCCAGTCATCTTTATGA 343
QY	317	ATCAAAATGTAGGGGCTGCTTTGTGACGGAGTCCTTTCAGAGACATCAACGGGAAA 376
DB	344	ATCAAAATGTAGGGGCTGCTTTGTGACGGAGTCCTTTCAGAGACATCAACGGGAAA 403
QY	377	GAGAAAGACATTCACCTTGGAGGGCTCTTGTGAAATGGTTAACTCTCCTTTTGGCC 436
DB	404	GAGAAAGACATTCACCTTGGAGGGCTCTTGTGAAATGGTTAACTCTCCTTTTGGCC 463
QY	437	AGTCACACAGCTGACCTACATCTTTTAGTACAAATGGAGTGCGCTTGTAGC 496
DB	464	AGTCACACAGCTGACCTACATCTTTTAGTACAAATGGAGTGCGCTTGTAGC 523
QY	497	ACACACCATTAATCATCATCTGTCGCAATTAAGAGAGGCTGGAAAGAGACATTAATG 556
DB	524	ACACACCATTAATCATCATCTGTCGCAATTAAGAGAGGCTGGAAAGAGACATTAATG 583
QY	557	TTGTATGCGCCATGAGATGAGTGGAACTCAATTTTACTGAGAGGTGGTCTTGC 616
DB	584	TTGTATGCGCCATGAGATGAGTGGAACTCAATTTTACTGAGAGGTGGTCTTGC 643
QY	617	TGGAAGTGAACGGAAAGTCTCTTAATGATAGCCGCCATTTGTGGAATCAATA 676
DB	644	TGGAAGTGAACGGAAAGTCTCTTAATGATAGCCGCCATTTGTGGAATCAATA 703
QY	677	CATCCACATTTTGGAGCCATTAATCACTGCTCCAAAGCTTATGAGCGAAGTTGC 736
DB	704	CATCCACATTTTGGAGCCATTAATCACTGCTCCAAAGCTTATGAGCGAAGTTGC 763
QY	737	AACAGGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGGAAACATAAGGTTGACA 796
DB	764	AACAGGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGGAAACATAAGGTTGACA 823
QY	797	TTGATTCAGTCAGAGGTTGTAGTTTACATCAAAAGCTCCCAAGATGTGCTCTCTCT 856
DB	824	TTGATTCAGTCAGAGGTTGTAGTTTACATCAAAAGCTCCCAAGATGTGCTCTCTCT 883
QY	857	CTTCAGACTGTTTCTCACTGTAATCTTCTGGGTAACTGGAGAGAGCTTCAACTCTGTC 916
DB	884	CTTCAGACTGTTTCTCACTGTAATCTTCTGGGTAACTGGAGAGAGCTTCAACTCTGTC 943
QY	917	ACCTGCTTTCG----- 926
DB	944	ACCTGCTTTCGAGGTGGTGTGCTGAGTTCTCTCGTTGTTTCCCTGGCTCTCTGTGAGGAA 1003
QY	927	----- 926
DB	1004	AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGTCTTACCTGTGCGCAACATGGGCG 1063
QY	927	-----AGGAGC 932
DB	1064	CAACCCGAAATCTTCCCAATCTTTATCTTGGCTGGCAGCGAGATGCTCAACAAGGAGC 1123

QY	933	TGATGACGACGAATGGGATGTGTTATGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 992
DB	1124	TGATGACGACGAATGGGATGTGTTATGTTAAATGCCAGCAATACCTGTCCAAAGCCTG 1183
QY	993	ACTTTATCCCCAGTCTCATTTCCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAA 1052
DB	1184	ACTTTATCCCCAGTCTCATTTCCCTGCGTGTGCCTGTGAATGACAGCTTTTGTGAGAAA 1243
QY	1053	TTTTGCGGTGGTTGGACAAATCAGTAGATTTTCATTGAGAAAAGCAAGCCCTCCATGGAT 1112
DB	1244	TTTTGCGGTGGTTGGACAAATCAGTAGATTTTCATTGAGAAAAGCAAGCCCTCCATGGAT 1303
QY	1113	GTGTTCTAGTGACACTGTTTAGCTGGGATCTCCCGTCCGCCACCATCGCTATCGCTACA 1172
DB	1304	GTGTTCTAGTGACACTGTTTAGCTGGGATCTCCCGTCCGCCACCATCGCTATCGCTACA 1363
QY	1173	TCATGAAGAGGATGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAGAGAC 1232
DB	1364	TCATGAAGAGGATGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAGAGAC 1423
QY	1233	CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTCGACTATGAGAAAGAGATTA 1292
DB	1424	CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTCGACTATGAGAAAGAGATTA 1483
QY	1293	AGAACAGACTCGAGCATCAGGGCCAAAGACAACTCAAGCTGCTGCACCTGGAGAAGC 1352
DB	1484	AGAACAGACTCGAGCATCAGGGCCAAAGACAACTCAAGCTGCTGCACCTGGAGAAGC 1543
QY	1353	CAATGAACCTCTCCTGCTGCTCAGAGGTTGGACAGAAAAGCGAGCGCCCTCAGTC 1412
DB	1544	CAATGAACCTCTCCTGCTGCTCAGAGGTTGGACAGAAAAGCGAGCGCCCTCAGTC 1603
QY	1413	CACCTGTGCCGACTCTGCTACCTCAGAGGCGAGGACAAAGGCCCGTGTGATCCCGCA 1472
DB	1604	CACCTGTGCCGACTCTGCTACCTCAGAGGCGAGGACAAAGGCCCGTGTGATCCCGCA 1663
QY	1473	GGGTGCCAGCTGCGCAGCGTGAGCGCTGCTGTTAGAGGACAGCGCGCTGTACAGG 1532
DB	1664	GGGTGCCAGCTGCGCAGCGTGAGCGCTGCTGTTAGAGGACAGCGCGCTGTGTACAGG 1723
QY	1533	CGTCTAGTGGGTGACCTGCTCCGACAGACAGCTGGAAGACAGCAATAAGCTCAAGCGTT 1592
DB	1724	CGTCTAGTGGGTGACCTGCTCCGACAGACAGCTGGAAGACAGCAATAAGCTCAAGCGTT 1783
QY	1593	CGTCTCTCTGATATCAAAATCAGTTTCAATTCAGCAGCATGGCAGCATCTTACATG 1652
DB	1784	CGTCTCTCTGATATCAAAATCAGTTTCAATTCAGCAGCATGGCAGCATCTTACATG 1843
QY	1653	GCTTCTCTCATCAGAGATGCTTTGGAACTACTACAAACCTTCCACTACTCTGATGGGA 1712
DB	1844	GCTTCTCTCATCAGAGATGCTTTGGAACTACTACAAACCTTCCACTACTCTGATGGGA 1903
QY	1713	CCAAAGCTATGCCAGTTCTCCCTGTTTCAGGAATATTCGGAGCAGACTCCCGAAACCA 1772
DB	1904	CCAAAGCTATGCCAGTTCTCCCTGTTTCAGGAATATTCGGAGCAGACTCCCGAAACCA 1963
QY	1773	GTCTGATTAAGAGGAGGACCATCCCAAGAGCTGCGACGCCAGCGGCTTCAGACA 1832
DB	1964	GTCTGATTAAGAGGAGGACCATCCCAAGAGCTGCGACGCCAGCGGCTTCAGACA 2023
QY	1833	GCAGAGCAGGAGGATTTGCAATTCGGTCAGAACCCAGCAGAGTGGCACCGCCAGAGGTCCC 1892
DB	2024	GCAGAGCAGGAGGATTTGCAATTCGGTCAGAACCCAGCAGAGTGGCACCGCCAGAGGTCCC 2083
QY	1893	TTTTATCTCACTGCATCGAAGTGGAGGCTGGAGGACAAATTAACACAGAGCTTCTTTT 1952
DB	2084	TTTTATCTCACTGCATCGAAGTGGAGGCTGGAGGACAAATTAACACAGAGCTTCTTTT 2143
QY	1953	TCCGCGCTTTTCCACCGAGCAGCAGCACTTCAAGAGTCTGCTGGCTGGGCTTAAAGGCT 2012
DB	2144	TCCGCGCTTTTCCACCGAGCAGCAGCACTTCAAGAGTCTGCTGGCTGGGCTTAAAGGCT 2203
QY	2013	GGCACTCGGATATCTTTGGCCCCCAGAGACTCTACCCCTTCCCTGACAGAGCTGGTATT 2072

3283 CCAATCCAACTGCTATGCACAAATATCCCTGGGCTAGATGGAGATAATTTTTTTT 3343
 3153 CTTCTCAGCTTTATGAAGAGAGGGGAACTGTCTAGGATTCACTGTAACACACAGGAACC 3212
 3343 CTTCTCAGCTTTATGAAGAGAGGGGAACTGTCTAGGATTCACTGTAACACACAGGAACC 3402
 3213 TGGCAACATCACGATTTAAGCTTAAGTTGGGAGGCTTAACGAGTCTACCTCCCTCTTTGTA 3272
 3403 TGGCAACATCACGATTTAAGCTTAAGTTGGGAGGCTTAACGAGTCTACCTCCCTCTTTGTA 3462
 3273 AATCAAGAATTTGTTTAAATGGCAATGTCATCTCTTTAAATAAAGATGAACCTTGGTTTC 3332
 3463 AATCAAGAATTTGTTTAAATGGCAATGTCATCTCTTTAAATAAAGATGAACCTTGGTTTC 3522
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 ABV21092
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 AC ABV21092;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21083.
 XX
 DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 KW Homo sapiens.
 OS
 PN WO200150860-A2.
 PD 23-AUG-2001.
 PP 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 3485; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Gaps 2;

197 GCTTT CAGTCCAGTGTAAAGCTGTTGGAGCGCGGAGCAAAAGGTAAGAATGATGTAATG 256 QY
224 GCTTT CAGTCCAGTGTAAAGCTGTTGGAGCGCGGAGCAAAAGGTAAGAATGATGTAATG 283 Db
257 CGTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATTCCAGTCACTCTCTTTATGA 316 QY
284 CGTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATTCCAGTCACTCTCTTTATGA 343 Db
317 ATCAAAATGAGGGGTGCTTTTGTGAGCGAGTCCCTTTGCAAGAGCACATCAACGGGAAA 376 QY
344 ATCAAAATGAGGGGTGCTTTTGTGAGCGAGTCCCTTTGCAAGAGCACATCAACGGGAAA 403 Db
377 GAGAAAGAGACATTCACCTTGGAGGGCTCTTCTGGAATGGTTTAACTCTCTTTTGGCC 436 QY
404 GAGAAAGAGACATTCACCTTGGAGGGCTCTTCTGGAATGGTTTAACTCTCTTTTGGCC 463 Db
437 AGTCACCAACGAGCTGACCTCATACACTTTTATGTAACAATGGAGTGGCTTGAGCCTTGAGC 496 QY
464 AGTCACCAACGAGCTGACCTCATACACTTTTATGTAACAATGGAGTGGCTTGAGCCTTGAGC 523 Db
497 ACACCAACCTATCATCTGTCGAATTAAGAAGGAGTGGGAAGAGAGACTTATG 556 QY
524 ACACCAACCTATCATCTGTCGAATTAAGAAGGAGTGGGAAGAGAGACTTATG 583 Db
557 TTGTCTATGGCCCATGAGATGATGGAACCTCAAAATGTTACTGAGAGGTTGGTGGCTTGC 616 QY
584 TTGTCTATGGCCCATGAGATGATGGAACCTCAAAATGTTACTGAGAGGTTGGTGGCTTGC 643 Db
617 TGGAAAGTGAACGGAAAAGTCTCTTAATGATAGCGGCATTTGGAATACATA 676 QY
644 TGGAAAGTGAACGGAAAAGTCTCTTAATGATAGCGGCATTTGGAATACATA 703 Db
677 CATCCCACTTTTGGAAAGCATTAAATCAACTGCTCCAAAGCTTATGAGCGGAAGGTTGC 736 QY
704 CATCCCACTTTTGGAAAGCATTAAATCAACTGCTCCAAAGCTTATGAGCGGAAGGTTGC 763 Db
737 AACAGGCAAAAGTGTAAATPACAGAGCTCATCCAGCAITTCAGCGAAACATAGGTTGACA 796 QY
764 AACAGGCAAAAGTGTAAATPACAGAGCTCATCCAGCAITTCAGCGAAACATAGGTTGACA 823 Db
797 TTGATTCAGTCCAGAGGTTGATGTTAGTATCAAGCTCCCAAGCTTCCAGATGTTGCTCTCT 856 QY
824 TTGATTCAGTCCAGAGGTTGATGTTAGTATCAAGCTCCCAAGCTTCCAGATGTTGCTCTCT 883 Db
857 CTTCAGACTGTTTCTCACTGTACTTCTGGGTAACTGGAGAGAGCTTCAACTCTGTTTC 916 QY
884 CTTCAGACTGTTTCTCACTGTACTTCTGGGTAACTGGAGAGAGCTTCAACTCTGTTTC 943 Db
917 ACTGCTTGC----- 926 QY
944 ACTGCTTGCAGGTGGGTTTGTGAGTCTCTCGTTGTTTCCCTGGCTCTCTGTGAAGGAA 1003 Db
927 ----- 926 QY
1004 AATCCACTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAATTTGGC 1063 Db
927 -----AGGAGC 932 QY
1064 CAACCCGAATTCCTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGC 1123 Db
933 TGATTCAGAGCAATGGGATGTTGATGTTAAATGCCAGCAATACCTGTCMAAGGCTTG 992 QY
1124 TGATTCAGAGCAATGGGATGTTGATGTTAAATGCCAGCAATACCTGTCMAAGGCTTG 1183 Db
993 ACTTTATCCCGAGTCTCAATTCCTGCTGCTGTGGAATGACAGCTTTTGTGAGAAA 1052 QY
1184 ACTTTATCCCGAGTCTCAATTCCTGCTGCTGTGGAATGACAGCTTTTGTGAGAAA 1243 Db
1053 TTTTGGCGTGGTGGACAAATCAGTATTTCAATGGAAGCAAAAGGCTTCAATGGAT 1112 QY
1244 TTTTGGCGTGGTGGACAAATCAGTATTTCAATGGAAGCAAAAGGCTTCAATGGAT 1303 Db

1113 GTGTTCTAGTGCAGTCTGTTAGCTGGATCTCCGCTCCGCCACCATCGCTATCGCTACA 1172 QY
1304 GTGTTCTAGTGCAGTCTGTTAGCTGGATCTCCGCTCCGCCACCATCGCTATCGCTACA 1363 Db
1173 TCATGAAGAGGATGAGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAAGAAAGAC 1232 QY
1364 TCATGAAGAGGATGAGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAAGAAAGAC 1423 Db
1233 CTACTATATCTCCAAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAGAGATTA 1292 QY
1424 CTACTATATCTCCAAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAGAGATTA 1483 Db
1293 AGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTCTGCACCTGGAGAAGC 1352 QY
1484 AGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTCTGCACCTGGAGAAGC 1543 Db
1353 CAAATGAACCTGTCCTCTCTCAGAGGCTGACAGAAAGCGAGACGCCCTCAGTC 1412 QY
1544 CAAATGAACCTGTCCTCTCTCAGAGGCTGACAGAAAGCGAGACGCCCTCAGTC 1603 Db
1413 CACCTCTGTGCCGACTCTCTACTCTCAGAGGCGAGGACAAAGGCCGCTGCATCCGCCA 1472 QY
1604 CACCTCTGTGCCGACTCTCTACTCTCAGAGGCGAGGACAAAGGCCGCTGCATCCGCCA 1663 Db
1473 GGTGCCAGAGCTGCCAGCTGAGCGCTGCTGTTAGAGGACAGCCCGCTGTACAGG 1532 QY
1664 GGTGCCAGAGCTGCCAGCGCTGAGCGCTGCTGTTAGAGGACAGCCCGCTGTGTACAGG 1723 Db
1533 CGCTCAGTGGGCTGCACCTGTCGCGAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1592 QY
1724 CGCTCAGTGGGCTGCACCTGTCGCGAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1783 Db
1593 CTTTCTCTCGATATCAAACTCAGTTTCATTTAGCCAGCATGGCAGCATCTTACATG 1652 QY
1784 CTTTCTCTCGATATCAAACTCAGTTTCATTTAGCCAGCATGGCAGCATCTTACATG 1843 Db
1653 GCTTCTCCTCATCAGAAGATGCTTTGGAAATACTACAACTTTCCACTACTCTGATGGGA 1712 QY
1844 GCTTCTCCTCATCAGAAGATGCTTTGGAAATACTACAACTTTCCACTACTCTGATGGGA 1903 Db
1713 CCAACAAGCTATGCCAGTTTCTCCCTGTTTCAGGAACCTATCGGAGCAGACTCCCGAAACCA 1772 QY
1904 CCAACAAGCTATGCCAGTTTCTCCCTGTTTCAGGAACCTATCGGAGCAGACTCCCGAAACCA 1963 Db
1773 GTCTGATTAAGAGAGAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTTCAGACA 1832 QY
1964 GTCTGATTAAGAGAGAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTTCAGACA 2023 Db
1833 GCCAGAGCAAGGATTTGCAATTCGGTTCAGAACCCAGCAGAGTGGCACCCGCCAGAGTCCC 1892 QY
2024 GCCAGAGCAAGGATTTGCAATTCGGTTCAGAACCCAGCAGAGTGGCACCCGCCAGAGTCCC 2083 Db
1893 TTTTATCTCAGTGCATCGAAGTGGAGGGTGGAGGACAAATTACCACACAGCTTCCCTTT 1952 QY
2084 TTTTATCTCAGTGCATCGAAGTGGAGGGTGGAGGACAAATTACCACACAGCTTCCCTTT 2143 Db
1953 TCGGCTCTTCCACAGCAGCAGCACCTTCACGAAGTCTGCTGGCTGGGCTTAAAGGCT 2012 QY
2144 TCGGCTCTTCCACAGCAGCAGCACCTTCACGAAGTCTGCTGGCTGGGCTTAAAGGCT 2203 Db
2013 GGCACCTCGGATATCTTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTATT 2072 QY
2204 GGCACCTCGGATATCTTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTATT 2263 Db
2073 TTGCCACAGAGTCTCCACACTTCTACTCTGCTCAGCCATCTACGAGGAGCAGTGGCAGTT 2132 QY
2264 TTGCCACAGAGTCTCCACACTTCTACTCTGCTCAGCCATCTACGAGGAGCTGGCAGTT 2323 Db
2133 ACTCTGCTACAGCTCAGCAGCTGCCCACTTTGGCGGAGACCAAGTCTATTCTGTGGGGA 2192 QY
2324 ACTCTGCTACAGCTCAGCAGCTGCCCACTTTGGCGGAGACCAAGTCTATTCTGTGGGCA 2383 Db
2193 GCGGCGAAGACCAAGTGACAGAGCTGACTCGCGGGGAGCTGGCATGAAGAGAGACCCCT 2252 QY

Db 2384 GCGCGCAGAGCCAGTGCACAGAGCTGACTCGCGCGGAGCTGCGATGAAAGAGAGCCCTT 2443
QY 2253 TTGAAGACAGTTTAAACGACAGAGCTGCCAAATTTGGAGAGAGCATCATGTCTAG 2312
Db 2444 TTGAAGACAGTTTAAACGACAGAGCTGCCAAATTTGGAGAGAGCATCATGTCTAG 2503
QY 2313 AGAACAGGTCTACGGGAAGAGCTGGGGAAAGTGGGAGTCTAGCTTTTGGGAGCA 2372
Db 2504 AGAACAGGTCTACGGGAAGAGCTGGGGAAAGTGGGAGTCTAGCTTTTGGGAGCA 2563
QY 2373 TGGAAATCATTTGAGGTCTCTGAGAGAAAGACACTTGTGACTTCTATACAAATTTTT 2432
Db 2564 TGGAAATCATTTGAGGTCTCTGAGAGAAAGACACTTGTGACTTCTATACAAATTTTT 2623
QY 2433 TTTCTTTGTTCACAAAAAATTTCCCTGTAATTTCTGAATATATATATATATATATAT 2492
Db 2624 TTTCTTTGTTCACAAAAAATTTCCCTGTAATTTCTGAATATATATATATATATATAT 2683
QY 2493 ATTTTGTGAAATGAGCTATGTTGTAAGACACAGGTGGATCAACCCAGTTGTTACTC 2552
Db 2684 ATTTTGTGAAATGAGCTATGTTGTAAGACACAGGTGGATCAACCCAGTTGTTACTC 2743
QY 2553 TCTTAACATCTGCATTTTTCAGAGATCAGCTAATCTCTCAACAAAAATGGAAGGCGAG 2612
Db 2744 TCTTAACATCTGCATTTTTCAGAGATCAGCTAATCTCTCAACAAAAATGGAAGGCGAG 2803
QY 2613 ATGCTAGAAATCCCTTCAGAGAGGAGAAACCATTTTATTCAGTGAATACATCTCTCT 2672
Db 2804 ATGCTAGAAATCCCTTCAGAGAGGAGAAACCATTTTATTCAGTGAATACATCTCTCT 2863
QY 2673 TGTTCCTAAAAAGCAAGTGTCTTGTGTGTGGAGACAAAAATCCCTACCATTTTCCAC 2732
Db 2864 TGTTCCTAAAAAGCAAGTGTCTTGTGTGTGGAGACAAAAATCCCTACCATTTT-CAC 2922
QY 2733 GTTGTGCTACTAAGAGATCTCAATATATTAAGTCTTTGTCGGAACCTTCCATAGTACACCT 2792
Db 2923 GTTGTGCTACTAAGAGATCTCAATATATTAAGTCTTTGTCGGAACCTTCCATAGTACACCT 2982
QY 2793 TAGCCCTCAGACTGAGCAGCTTGGGGGTGAGGTAGTACCTGTGAGGACAGAGCC 2852
Db 2983 TAGCCCTCAGACTGAGCAGCTTGGGGGTGAGGTAGTACCTGTGAGGACAGAGCC 3042
QY 2853 TAGTGGTAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCACC 2912
Db 3043 TAGTGGTAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCACC 3102
QY 2913 TGACAGCGAGGACACAGCATCACTCTGTCGACGACCATTAGGGGCTTCCCAAGG 2972
Db 3103 TGACAGCGAGGACACAGCATCACTCTGTCGACGACCATTAGGGGCTTCCCAAGG 3162
QY 2973 TCTACCTTTAGAGCAACCCAGTACCTCAGACAGGAAAGTGGGGCTTTGACCACTACCAT 3032
Db 3163 TCTACCTTTAGAGCAACCCAGTACCTCAGACAGGAAAGTGGGGCTTTGACCACTACCAT 3222
QY 3033 ATCTGGTAGCCCATTTTCTAGGCAATTTGGAATAGGTAGGTAGTACACATTTTCAGA 3092
Db 3223 ATCTGGTAGCCCATTTTCTAGGCAATTTGGAATAGGTAGGTAGTACACATTTTCAGA 3282
QY 3093 CCAATTTCAAACTGTCTATGCACAAAATTTCCCGTGGGCTAGATGGAGATAATTTTTTTT 3152
Db 3283 CCAATTTCAAACTGTCTATGCACAAAATTTCCCGTGGGCTAGATGGAGATAATTTTTTTT 3342
QY 3153 CTTCTCAGCTTTATGAAGAGAGGAAATCTGCTAGGATTCAGCTGAACCAACAGGAACC 3212
Db 3343 CTTCTCAGCTTTATGAAGAGAGGAAATCTGCTAGGATTCAGCTGAACCAACAGGAACC 3402
QY 3213 TGGCAACATCAGATTTTAAGCTAAGTTGGGAGCTAACGAGTCTACCTCCCTCTTTGA 3272
Db 3403 TGGCAACATCAGATTTTAAGCTAAGTTGGGAGCTAACGAGTCTACCTCCCTCTTTGA 3462
QY 3273 AATCAAGAAATGTTTAAATGGGATTTGTCAATCCTTTTAAATAAGATGAATCGTTTC 3332

Db 3463 AATCAAGAAATGTTTAAATGGGATTTGTCAATCCTTTTAAATAAGATGAATCGTTTC 3522
RESULT 13
ABV21312
ID ABV21312 standard; cDNA; 5145 BP.
XX AC ABV21312;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 21303.
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW Pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 3539; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
Query Match 88.5%; Score 2950; DB 5; Length 5145;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;
QY 197 GCTTTTCAGTCCAGTGTAAAGCTCTTGGAGCGCGGAGCAAGGTAAGATGATGTAATG 256
Db 224 GCTTTTCAGTCCAGTGTAAAGCTCTTGGAGCGCGGAGCAAGGTAAGATGATGTAATG 283
QY 257 CGCTGGGTGCTCCAAAGCATCTTTTGTGTGGAATGTTATTCAGTCTCTCTTTATGA 316
Db 284 CGCTGGGTGCTCCAAAGCATCTTTTGTGTGGAATGTTATTCAGTCTCTCTTTATGA 343
QY 317 ATCAAAATGTGAGGGGCTGCTTTGTGACGGAGTCTTTGCAAGAGCACATCAACGGAAA 376
Db 344 ATCAAAATGTGAGGGGCTGCTTTGTGACGGAGTCTTTGCAAGAGCACATCAACGGAAA 403

QY 377 GAGAAAGACAAATTCACCTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGGC 436
DB 404 GAGAAAGACAAATTCACCTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGGC 463
QY 437 AGTCACACAGCTTGACCTCATACACTTTTGTAGTAACTAGAGTGGCTTGAGCCTTTGAGC 496
DB 464 AGTCACACAGCTTGACCTCATACACTTTTGTAGTAACTAGAGTGGCTTGAGCCTTTGAGC 523
QY 497 ACACCAACCAATTCATCATCGTGGGAAAATTAAGAAGGAGGTGGGAAAAGAGGACTTATTG 556
DB 524 ACACCAACCAATTCATCATCGTGGGAAAATTAAGAAGGAGGTGGGAAAAGAGGACTTATTG 583
QY 557 TTGTCTATGCCCATGAGATGTTGAACTCAAAATGTTACTGAGAGGTTGTTGCTCTGCG 616
DB 584 TTGTCTATGCCCATGAGATGTTGAACTCAAAATGTTACTGAGAGGTTGTTGCTCTGCG 643
QY 617 TGGAAAGTGGAAACGGAAAAGTGTCTCTAATTGATAGCGGCCAATTTGTGGAATACAAATA 676
DB 644 TGGAAAGTGGAAACGGAAAAGTGTCTCTAATTGATAGCGGCCAATTTGTGGAATACAAATA 703
QY 677 CATCCACAAATTTGGAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGC 736
DB 704 CATCCACAAATTTGGAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGC 763
QY 737 AACAGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAAACATAAGGTTGACA 796
DB 764 AACAGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAAACATAAGGTTGACA 823
QY 797 TTGATTTGAGTCAGAGGTTGTAGTTTACGATCAAGCTCCAGAGTTTGCCTCTCT 856
DB 824 TTGATTTGAGTCAGAGGTTGTAGTTTACGATCAAGCTCCAGAGTTTGCCTCTCT 883
QY 857 CTTTCAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGGCTTCAACTCTGTT 916
DB 884 CTTTCAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAAGGCTTCAACTCTGTT 943
QY 917 ACTGCTTGC----- 926
DB 944 ACTGCTTGCAGGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAA 1003
QY 927 ----- 926
DB 1004 AATCCACTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACTGTTGCGCAACATTTGGC 1063
QY 927 -----AGGAGC 932
DB 1064 CAACCCGAATTTCTCCAAATCTTATCTTGGCTGCCAGCGAGATGCTCCTCAACAGGAGC 1123
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DB 1124 TGATGAGAGGATGGGATTTGTTATGCTTAAATGCCAGCAATACCTGTCCAAAGCTG 1183
QY 993 ACTTTATCCCGAGTCTCAATTTCTCGCTGTGCTGTGTAATGACAGCTTTTGTGAGAAA 1052
DB 1184 ACTTTATCCCGAGTCTCAATTTCTCGCTGTGCTGTGTAATGACAGCTTTTGTGAGAAA 1243
QY 1053 TTTTGGCTGGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCCTCCAAATGAT 1112
DB 1244 TTTTGGCTGGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCCTCCAAATGAT 1303
QY 1113 GTGTTCTAGTGCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCACCAATCGCTATCGCCTACA 1172
DB 1304 GTGTTCTAGTGCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCACCAATCGCTATCGCCTACA 1363
QY 1173 TCATGAAGAGGATGGACATGCTCTTTTGTAGTAGAGCTTACAGATTTGTGAAAGAAAAGAC 1232
DB 1364 TCATGAAGAGGATGGACATGCTCTTTTGTAGTAGAGCTTACAGATTTGTGAAAGAAAAGAC 1423
QY 1233 CTACTATCTCCAAATTTCTGGGCCAACTCTCGACTATGAGAAAGAGATTA 1292
DB 1424 CTACTATCTCCAAATTTCTGGGCCAACTCTCGACTATGAGAAAGAGATTA 1483

QY 1293 AGAACCAAGCTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1352
DB 1484 AGAACCAAGCTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAGC 1543
QY 1353 CAAATGAACTGTTCCCTGCTGTCTCAGAGGTTGACAGAAAAGGAGACGCCCTCTCAGTC 1412
DB 1544 CAAATGAACTGTTCCCTGCTGTCTCAGAGGTTGACAGAAAAGGAGACGCCCTCTCAGTC 1603
QY 1413 CACCTGTGGCGACTCTGTACTCCTCAGAGCAGCAGGACAAAGGCCGCTGCATCCCGCCA 1472
DB 1604 CACCTGTGGCGACTCTGTACTCCTCAGAGGACAGGACAAAGGCCGCTGCATCCCGCCA 1663
QY 1473 GCGTCCCGCAGCGTGCACAGCGTGCAGCGTGTGTTTGTAGAGGACAGCCCTCTGTTACAGG 1532
DB 1664 GCGTCCCGCAGCGTGCACAGCGTGCAGCGTGTGTTTGTAGAGGACAGCCCTCTGTTACAGG 1723
QY 1533 CGCTCAGTGGGCTGCACCTGTCCGACAGCAGGCTGGAAGACGCAATAAGCTCAAGCGTT 1592
DB 1724 CGCTCAGTGGGCTGCACCTGTCCGACAGCAGGCTGGAAGACAGCAATAAGCTCAAGCGTT 1783
QY 1593 CCTTCTCTCTGGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATG 1652
DB 1784 CCTTCTCTCTGGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATG 1843
QY 1653 GCTTCTCTCATCAGAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATGGGA 1712
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DB 1904 CCAACAAAGCTATGCCAGTTCTCCCTGTTTCAAGAACTATCGGAGCAGACTCCCGAAACCA 1963
QY 1773 GTCTGTATAAGAGGAAAGCCAGCATTCCTCCAAAGAGCTGCGAGACGCCAGGCTTCAGACA 1832
DB 1964 GTCTGTATAAGAGGAAAGCCAGCATTCCTCCAAAGAGCTGCGAGACGCCAGGCTTCAGACA 2023
QY 1833 GCCAGACAAAGGATGTCATTCGCTGAGAACCCAGCAGTGCCACGCCAGAGGTCCC 1892
DB 2024 GCCAGACAAAGGATGTCATTCGCTGAGAACCCAGCAGTGCCACGCCAGAGGTCCC 2083
QY 1893 TTTTATCTCCACTGCATCGAAAGTGGAGCGTGGAGGACAAATTACCAACAGCTTCCTTT 1952
DB 2084 TTTTATCTCCACTGCATCGAAAGTGGAGCGTGGAGGACAAATTACCAACAGCTTCCTTT 2143
QY 1953 TCGGCTTTCCACAGCAGCAGCAGCAGCTCAGAGTCTGCTGGCTGGCTGGCTTAAAGGCT 2012
DB 2144 TCGGCTTTCCACAGCAGCAGCAGCAGCTCAGAGTCTGCTGGCTGGCTGGCTTAAAGGCT 2203
QY 2013 GGCACCTCGGATATCTTGGCCCCCAGAGCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2072
DB 2204 GGCACCTCGGATATCTTGGCCCCCAGAGCTCTACCCCTTCCCTGACCAGCAGCTGGTATT 2263
QY 2073 TTGCCACAGAGTCTCACAATTTACTTCTGCTCAGCCATCTACGGAGGAGTCCAGTT 2132
DB 2264 TTGCCACAGAGTCTCACAATTTACTTCTGCTCAGCCATCTACGGAGGAGTCCAGTT 2323
QY 2133 ACTCTGCTTACAGCTGACAGCAGCTGCCACTTCCGGAGACCAAGTCTATTCTGTGGCA 2192
DB 2324 ACTCTGCTTACAGCTGACAGCAGCTGCCACTTCCGGAGACCAAGTCTATTCTGTGGCA 2383
QY 2193 GCGGACAGAAAGCAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAGAGAGCCCT 2252
DB 2384 GCGGACAGAAAGCAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAGAGAGCCCT 2443
QY 2253 TTGAAAGCAGTTTAAACGCAAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAG 2312
DB 2444 TTGAAAGCAGTTTAAACGCAAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAG 2503
QY 2313 AGHACAGGTTCACGGAAAGCTGGGAAAGTGGGAGTCACTCTAGCTTTTTCGGGAGCA 2372
DB 2504 AGHACAGGTTCACGGAAAGCTGGGAAAGTGGGAGTCACTCTAGCTTTTTCGGGAGCA 2563
QY 2373 TGGAAATCAATTGAGGTCTCTCTGAGAGGAAAGACACTTGTGACTTCTATAGACAAATTTTT 2432

2564 TGGAAATCATTGAGTCTCCTGAGAGAGAACACATTGTGACTCTATAGCAATTTTT 2623
2433 TTCTTGTTCACAAAAAATTCCTGTAATCTGAATAATATATATATGATACATATAT 2492
2624 TTCTTGTTCACAAAAAATTCCTGTAATCTGAATAATATATATATGATACATATAT 2683
2493 ATTTTGGAAAAATGGAGTATGTTGTTGTAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2552
2684 ATTTTGGAAAAATGGAGTATGTTGTTGTAAGCAACAGGTGGATCAACCCAGTTGTTACTC 2743
2553 TCTTAACATCTGCATTTGAGAGATCAGCTAATCTCTCAACAAAAATGGAAGGAG 2612
2744 TCTTAACATCTGCATTTGAGAGATCAGCTAATCTCTCAACAAAAATGGAAGGAG 2803
2613 ATGCTAGAAATCCCCCTAGAGCGAGGAAAAACCAATTTTATTCAGTGAATTACACATCTCT 2672
2804 ATGCTAGAAATCCCCCTAGAGCGAGGAAAAACCAATTTTATTCAGTGAATTACACATCTCT 2863
2673 TGTTCCTTAAGAAAGCAAGTGTCTTTGTTGTTGAGGACAAATCCCTACCATTTTCCAC 2732
2864 TGTTCCTTAAGAAAGCAAGTGTCTTTGTTGTTGAGGACAAATCCCTACCATTTT-CAC 2922
2733 GTTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCGGAACCTTCCATAGTACACCT 2792
2923 GTTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCGGAACCTTCCATAGTACACCT 2982
2793 TAGGCTGAGACTGAGCCAGCTTGGGGGTGAGGTAGTACACCTGTTAGGAGACAGAGCC 2852
2983 TAGGCTGAGACTGAGCCAGCTTGGGGGTGAGGTAGTACACCTGTTAGGAGACAGAGCC 3042
2853 TAGTGTGTAATCCAAAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCAC 2912
3043 TAGTGTGTAATCCAAAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCAC 3102
2913 TGACAGCGAGGACACGAGCATCACTCTGCTGGAACGACATAGGGGCTTGGCAAGG 2972
3103 TGACAGCGAGGACACGAGCATCACTCTGCTGGAACGACATAGGGGCTTGGCAAGG 3162
2973 TCTACCTTAGAGCAACCCAGTACTCAGACAGGAGAGTGGGGCTTGGCAACTACCAT 3032
3163 TCTACCTTAGAGCAACCCAGTACTCAGACAGGAGAGTGGGGCTTGGCAACTACCAT 3222
3033 ATCTGTTAGCCCATTTTCTAGGCAATTTGTAATAGGTAGTGTAGTCACTTTTTCAGA 3092
3223 ATCTGTTAGCCCATTTTCTAGGCAATTTGTAATAGGTAGTGTAGTCACTTTTTCAGA 3282
3093 CCAATTCAACTGTCTATGCAAAATTCCTGGGGCTAGATGGAGATATTTTTTTTT 3152
3283 CCAATTCAACTGTCTATGCAAAATTCCTGGGGCTAGATGGAGATATTTTTTTTT 3342
3153 CTCTCAGCTTTATGAGAGAGGAGAACTGTCTAGGATTCAGCTGAACCCAGGAAAC 3212
3343 CTCTCAGCTTTATGAGAGAGGAGAACTGTCTAGGATTCAGCTGAACCCAGGAAAC 3402
3213 TGGCAACTATCAGATTTAAGCTAAGTTGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
3403 TGGCAACTATCAGATTTAAGCTAAGTTGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462
3273 AATCAAGAAATTTTAAATAGGATTTGTCATCTTAAATTAAGATGAATTTGGTTTC 3332
3463 AATCAAGAAATTTTAAATAGGATTTGTCATCTTAAATTAAGATGAATTTGGTTTC 3522

RESULT 14
ABV21316
ID ABV21316 standard; cDNA; 5145 BP.
XX AC ABV21316;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 21307.

XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR C9-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA Schlegel R, Endege WO, Monahan JE;
XX PI WPI; 2001-662795/76.
XX DR Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PS Claim 1; Page 3540; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Query Match 88.5%; Score 2950; DB 5; Length 5145;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;
QY 197 GCTTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGAGCAAGGTAAGATGATGTAATG 256
Db 224 GCTTTTCAGTCCAGTGTAAAGCTGTTGGAGCGCGGAGCAAGGTAAGATGATGTAATG 283
QY 257 CGCTGGCTGCTCCAAAGCATCTTTGTTGGAAATGTTTCCAGTCTCTCTTTATGA 316
Db 284 CGCTGGCTGCTCCAAAGCATCTTTGTTGGAAATGTTTCCAGTCTCTCTTTATGA 343
QY 317 ATCAAAATGTGAGGGGCTGCTTTGTGGACGGAGTCTTTTGCAGAGCACATCAACGGGAA 376
Db 344 ATCAAAATGTGAGGGGCTGCTTTGTGGACGGAGTCTTTTGCAGAGCACATCAACGGGAA 403
QY 377 GAGAAAGACATTCACCTTGGAGGGCTCTTGTGAAATGGGTTTAACTCTCTCTTTGCC 436
Db 404 GAGAAAGACATTCACCTTGGAGGGCTCTTGTGAAATGGGTTTAACTCTCTCTTTGCC 453
QY 437 AGTCACCACCGAGCTGACCTACACCTTTTAGTACAAATGGAGTGGCTGAGCTTTGAGC 496
Db 464 AGTCACCACCGAGCTGACCTACACCTTTTAGTACAAATGGAGTGGCTGAGCTTTGAGC 523
QY 497 ACACACCATTCATCATCTGTCGCAAAATTAAGAGAGGTGGGAAAGAGGACTTTATTG 556
Db 524 ACACACCATTCATCATCTGTCGCAAAATTAAGAGAGGTGGGAAAGAGGACTTTATTG 583

QY	557	TTGTCATGCCCATGAGATGATTGGAATCAAAATGTTTACTGAGAGGTTGGTGCCTGCG	616
DB	584	TTGTATGCCCATGAGATGATTGGAATCAAAATGTTTACTGAGAGGTTGGTGCCTGCG	643
QY	617	TGGAAGTGGAGCGGAAAGTCTGCTAAATGATAGCGGCCATTTGTGGAATACAAATA	676
DB	644	TGGAAGTGGAGCGGAAAGTCTGCTAAATGATAGCGGCCATTTGTGGAATACAAATA	703
QY	677	CATCCACATTTTGAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGC	736
DB	704	CATCCACATTTTGAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGC	763
QY	737	AACAGGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATGAAGTTGACA	796
DB	764	AACAGGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATGAAGTTGACA	823
QY	797	TTGATTTGAGTCAAGAGGTTGATTTTACGATCAAAAGCTCCCAAGATGTTGCCTCTCTCT	856
DB	824	TTGATTTGAGTCAAGAGGTTGATTTTACGATCAAAAGCTCCCAAGATGTTGCCTCTCTCT	883
QY	857	CTTCAGACTGTTTCTCACTGTTCTCTGGTTAACTGGAGAAAGCTTCAACTCTGTTTC	916
DB	884	CTTCAGACTGTTTCTCACTGTTCTCTGGTTAACTGGAGAAAGCTTCAACTCTGTTTC	943
QY	917	ACCTGCTTGC-----	926
DB	944	ACCTGCTTGCAGTGGGTTGTGAGTCTCTGCTTGTGTTTCCCTGGCCTCTGTGAAGAA	1003
QY	927	-----	926
DB	1004	AATCCACTAGTCCCTACCTGCATTTCTCAGCCTTGTCTTACCTGTGTGCAACATTTGGC	1063
QY	927	-----	926
DB	1064	CAACCCGAAATCTCCCAATCTTTATCTTGTGCGCCAGCGAGATGCTCACAAGAGAC	1123
QY	933	TGATGACAGCAATGGGATTTGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCTG	992
DB	1124	TGATGACAGCAATGGGATTTGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCTG	1183
QY	993	ACTTTATCCCGAGTCTCATTTCTCTGGTGTGCTGTGAATGACAGCTTTTGTGAGAAA	1052
DB	1184	ACTTTATCCCGAGTCTCATTTCTCTGGTGTGCTGTGAATGACAGCTTTTGTGAGAAA	1243
QY	1053	TTTTGCCGTGGTTGGACAAATCAGTAGATTTCAATGAGAAAGCAAAAGCCTCCAAATGGAT	1112
DB	1244	TTTTGCCGTGGTTGGACAAATCAGTAGATTTCAATGAGAAAGCAAAAGCCTCCAAATGGAT	1303
QY	1113	GTGTTCTAGTGCACTGTTTATGCTGGATCTCCGCTCCGACCATCGCTATCGCTTACA	1172
DB	1304	GTGTTCTAGTGCACTGTTTATGCTGGATCTCCGCTCCGACCATCGCTATCGCTTACA	1363
QY	1173	TCATGAGAGGATGACATGTTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGAC	1232
DB	1364	TCATGAGAGGATGACATGTTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGAC	1423
QY	1233	CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTTGGACTATGAGAGAGATTA	1292
DB	1424	CTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTTGGACTATGAGAGAGATTA	1483
QY	1293	AGAACAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTCGGAGAGC	1352
DB	1484	AGAACAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTCGGAGAGC	1543
QY	1353	CAAAATGAACCTGTCCCTGCTGTCTCAGAGGTTGGACAGAAAGCGAGAGCGCCCTCAGTTC	1412
DB	1544	CAAAATGAACCTGTCCCTGCTGTCTCAGAGGTTGGACAGAAAGCGAGAGCGCCCTCAGTTC	1603
QY	1413	CACCTGTGCGACTCTCTCTACCTCAGAGGCGAGCAGCAAAAGCGCTGATCCGCCCA	1472
DB	1604	CACCTGTGCGACTCTCTCTACCTCAGAGGCGAGCAGCAAAAGCGCTGATCCGCCCA	1663

QY	1473	CGGTGCCAGCGTCCCGCAGCGTGCAGCGCTGTTAGAGGACAGCCCGCTGTTACAGG	1532
DB	1664	CGGTGCCAGCGTCCCGCAGCGTGCAGCGCTGTTAGAGGACAGCCCGCTGTTACAGG	1723
QY	1533	CGCTCAGTGGGCTGCACCTGTCCGACAGCAGGCTGGAAGACAGCAATAAGCTCAAGCGTT	1592
DB	1724	CGCTCAGTGGGCTGCACCTGTCCGACAGCAGGCTGGAAGACAGCAATAAGCTCAAGCGTT	1783
QY	1593	CGTTCTCTCTGGATATCAAAATCAGTTTCAATTTAGAGCAGTGCAGCATCTTTACATG	1652
DB	1784	CGTTCTCTCTGGATATCAAAATCAGTTTCAATTTAGAGCAGTGCAGCATCTTTACATG	1843
QY	1653	GGTTCTCTCTCATCAGAAGATCTTTTGAATACTACAAACCTTCCACTACTCTGGATGGGA	1712
DB	1844	GGTTCTCTCTCATCAGAAGATCTTTTGAATACTACAAACCTTCCACTACTCTGGATGGGA	1903
QY	1713	CCAAACAGCTATGCCAGTCTCCCTGTTTCCAGGAATCTTCCAGGACAGCTCCCGAAACCA	1772
DB	1904	CCAAACAGCTATGCCAGTCTCCCTGTTTCCAGGAATCTTCCAGGACAGCTCCCGAAACCA	1963
QY	1773	GTCTCTGATAAGGAGGAGGAGCCAGCATCCCAAGAGAGCTGCAGACCCGAGGCTTCAGACA	1832
DB	1964	GTCTCTGATAAGGAGGAGGAGCCAGCATCCCAAGAGAGCTGCAGACCCGAGGCTTCAGACA	2023
QY	1833	GGCAGAGCAAGGATGCTATTCGCTCAGAACCCAGCAGCTGGCAGCCGCGCAGAGGTCCTC	1892
DB	2024	GGCAGAGCAAGGATGCTATTCGCTCAGAACCCAGCAGCTGGCAGCCGCGCAGAGGTCCTC	2083
QY	1893	TTTTTATCTCCACTGCATCGAAAGTGGAGCGTGGAGGCAAAATACCAACACAGCTTCCTTT	1952
DB	2084	TTTTTATCTCCACTGCATCGAAAGTGGAGCGTGGAGGCAAAATACCAACACAGCTTCCTTT	2143
QY	1953	TGCGGCTTTTCCACAGGCGCAGCAGCACTCAGAAAGTCTGCTGGGCTTAAAGGCT	2012
DB	2144	TGCGGCTTTTCCACAGGCGCAGCAGCACTCAGAAAGTCTGCTGGGCTTAAAGGCT	2203
QY	2013	GGCACTCGGATATCTTGGCCCCCAGAGCTCTACCCCTTCCCTGACACAGAGCTGTAAT	2072
DB	2204	GGCACTCGGATATCTTGGCCCCCAGAGCTCTACCCCTTCCCTGACACAGAGCTGTAAT	2263
QY	2073	TTGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTGCAGTT	2132
DB	2264	TTGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTGCAGTT	2323
QY	2133	ACTCTGCTACAGCTGCAGCAGCTGCCACTTGGAGAGCCAAAGTCTATTCTGTGCGCA	2192
DB	2324	ACTCTGCTACAGCTGCAGCAGCTGCCACTTGGAGAGCCAAAGTCTATTCTGTGCGCA	2383
QY	2193	GGCGGACAGAGCCAAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGCCCT	2252
DB	2384	GGCGGACAGAGCCAAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGCCCT	2443
QY	2253	TTGAAAGCGATTTAAACCGCAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAG	2312
DB	2444	TTGAAAGCGATTTAAACCGCAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTGAG	2503
QY	2313	AGAACAGCTCAAGGAGAGCTGGGAAAGTGGGAGTGCAGTCTAGCTTTTGGGCGAGCA	2372
DB	2504	AGAACAGCTCAAGGAGAGCTGGGAAAGTGGGAGTGCAGTCTAGCTTTTGGGCGAGCA	2563
QY	2373	TGGAATCATTTGAGGCTCTCTGAGAGAGAGACACTTGTGACTTCTATAGACAAATTTT	2432
DB	2564	TGGAATCATTTGAGGCTCTCTGAGAGAGAGACACTTGTGACTTCTATAGACAAATTTT	2623
QY	2433	TTTCTTCTTCAAAAAAATTTCCCTGTAATCTGAAATATATATATATATATATATATAT	2492
DB	2624	TTTCTTCTTCAAAAAAATTTCCCTGTAATCTGAAATATATATATATATATATATATAT	2683
QY	2493	ATTTTTCGAAAAATGGAGCTATGTTGTAAGCAACAGGTGGATCAACCCAGTTGTTACTC	2552
DB	2684	ATTTTTCGAAAAATGGAGCTATGTTGTAAGCAACAGGTGGATCAACCCAGTTGTTACTC	2743
QY	2553	TCTTAAACATCTGCATTTGAGAGATCAGTAACTCTCTCAACAAAAATGGAAGGGCAG	2612

Db 2744 TCTTAAATCTGATTTGAGAGATCAGTAAATCTTCTCTCAACAAAATGGAAGGGCAG 2803
Qy 2613 ATGCTAGAAATCCCCCTAGACGAGGAAACCACTTTTATTCAGTGAATTAACATCCTCTCT 2672
Db 2804 ATGCTAGAAATCCCCCTAGACGAGGAAACCACTTTTATTCAGTGAATTAACATCCTCT 2863
Qy 2673 TGTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGACAAAATCCCTACCAATTTTCAC 2732
Db 2864 TGTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGACAAAATCCCTACCAATTTT-CAC 2922
Qy 2733 GTTCTGTACTTAAGAGATCTCAATA-TAGTCTTTGTCGGACCTTCCATAGTACACT 2792
Db 2923 GTTGTGTACTTAAGAGATCTCAATA-TAGTCTTTGTCGGACCTTCCATAGTACACT 2982
Qy 2793 TAGCGCTGAGATGAGCCAGCTTTGGGGTTCAGGTAGAGCCCTTTAGGACAGAGCC 2852
Db 2983 TAGCGCTGAGATGAGCCAGCTTTGGGGTTCAGGTAGAGCCCTTTAGGACAGAGCC 3042
Qy 2853 TAGTGGTAAATCCAGAGAAATGATCTATCCAAAGCTGATTCACAAACCCACGCTCAC 2912
Db 3043 TAGTGGTAAATCCAGAGAAATGATCTATCCAAAGCTGATTCACAAACCCACGCTCAC 3102
Qy 2913 TGACAGCCGAGGACACGAGCATCTCTCTGACGACCAATAGGGCCCTTGCACAGG 2972
Db 3103 TGACAGCCGAGGACACGAGCATCTCTCTGACGACCAATAGGGCCCTTGCACAGG 3162
Qy 2973 TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGAAAGTCGGGCTTTGACCACTACCAT 3032
Db 3163 TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGAAAGTCGGGCTTTGACCACTACCAT 3222
Qy 3033 ATCTGTAGTCCCAATTTCTAGGCAATTTGAAATAGTGTAGTGTAGTGTAGTGTAGTGTAG 3092
Db 3223 ATCTGTAGTCCCAATTTCTAGGCAATTTGAAATAGTGTAGTGTAGTGTAGTGTAGTGTAG 3282
Qy 3093 CCAATTCAAATGCTATGACAAATAATCCCTGGGCTAGATGAGAGATAATTTTTTTTT 3152
Db 3283 CCAATTCAAATGCTATGACAAATAATCCCTGGGCTAGATGAGAGATAATTTTTTTTT 3342
Qy 3153 CTCTCAGCTTTATGAAGAGAGGAAAGTCTAGGATTCAGCTCAACACACAGAAC 3212
Db 3343 CTCTCAGCTTTATGAAGAGAGGAAAGTCTAGGATTCAGCTCAACACACAGAAC 3402
Qy 3213 TGGCAACATACGATTTAAGCTAAGTTGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
Db 3403 TGGCAACATACGATTTAAGCTAAGTTGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462
Qy 3273 AATCAAGAAATGTTTAAATGGGATTTGCAATCCTTTAAATGAATGAATGATGTTTC 3332
Db 3463 AATCAAGAAATGTTTAAATGGGATTTGCAATCCTTTAAATGAATGAATGATGTTTC 3522

RESULT 15
ID ABV26826 standard; cDNA; 5145 BP.
XX AC ABV26826;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 26817.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX

PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
PI WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
PS Claim 1; Page 5420-5421; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
Query Match 88.5%; Score 2950; DB 5; Length 5145;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;
Qy 197 GCTTTCAGTCTCAGTGTAAAGCTGTTGGAGCGGGAGCAAGGTAAAGATGATTAATG 256
Db 224 GCCTTCAGTCCAGTGTAAAGCTGTTGGAGCGGGAGCAAGGTAAAGATGATTAATG 283
Qy 257 CGCTGGCTGCTCAAGAGCATCTTTGTTGGAATGTTATTCAGTCACTCTTTATGA 316
Db 284 CGTGGCTGCTCAAGAGCATCTTTGTTGGAATGTTATTCAGTCACTCTTTATGA 343
Qy 317 ATCAATGTGAGGGCTGCTTTGTGACGAGTCTTTGCAAGAGCACATCAACGGGAAA 376
Db 344 ATCAATGTGAGGGCTGCTTTGTGACGAGTCTTTGCAAGAGCACATCAACGGGAAA 403
Qy 377 GAGAAAGAGACATTCATCTTGGAGGGCTCTTGTGAAAATGGGTTTAACTCTCTTTGCC 436
Db 404 GAGAAAGAGACATTCATCTTGGAGGGCTCTTGTGAAAATGGGTTTAACTCTCTTTGCC 463
Qy 437 AGTCACCAACAGCTGACCTCATACACTTTTAGTACATGGAGTGGCTTGAGCCTTTGAGC 496
Db 464 AGTCACCAACAGCTGACCTCATACACTTTTAGTACATGGAGTGGCTTGAGCCTTTGAGC 523
Qy 497 ACACCAACCATTACATCATCGTGCAAAATTAAGAGAGGAGTGGGAAAAGAGACTTTATG 556
Db 524 ACACCAACCATTACATCATCGTGCAAAATTAAGAGAGGAGTGGGAAAAGAGACTTTATG 583
Qy 557 TTGTCATGGCCCATGAGATGATTTGGAACCTCAATTTTACTGAGAGTTGGTGGCTCTGC 616
Db 584 TTGTCATGGCCCATGAGATGATTTGGAACCTCAATTTTACTGAGAGTTGGTGGCTCTGC 643
Qy 617 TGGAAAGTGAACCGGAAAAGTCTCTTAATGATAGCCGCCATTTGTGGAATACAATA 676
Db 644 TGGAAAGTGAACCGGAAAAGTCTCTTAATGATAGCCGCCATTTGTGGAATACAATA 703
Qy 677 CATCCCACTTTTGGAGGCCATTAATATCACTGCTCAAGCTTATGAGCGAAGGTGC 736
Db 704 CATCCCACTTTTGGAGGCCATTAATATCACTGCTCAAGCTTATGAGCGAAGGTGC 763

QY	737	AACAGGACAAAGTGTTAAATACAGAGCTCATCCAGCAATTCAGCGAAACATACAGGTTGACA	796
Db	764	AACAGGACAAAGTGTTAAATACAGAGCTCATCCAGCAATTCAGCGAAACATACAGGTTGACA	823
QY	797	TTGATTGACAGTCAGAGGTTGTAGTTTACAGTCAAAAGCTCCCAAGATGTTGCTCTCTCT	856
Db	824	TTGATTGACAGTCAGAGGTTGTAGTTTACAGTCAAAAGCTCCCAAGATGTTGCTCTCTCTCT	883
QY	857	CTTACAGATGTTTCTCACTGTATCTCTGTTGTTAACTGAGGAGAGCTTCAACTCTGTTC	916
Db	884	CTTACAGATGTTTCTCACTGTATCTCTGTTGTTAACTGAGGAGAGCTTCAACTCTGTTC	943
QY	917	ACCTGCTTGC-----	926
Db	944	ACCTGCTTGCAGGTGGTTGCTGAGTTCTCTGTTGTTCCCTGGGCTCTGTGAAGGAA	1003
QY	927	-----	926
Db	1004	AATCCACTCTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACCTGTTGCCAACATTTGGGC	1063
QY	927	-----	932
Db	1064	CAACCGCAATCTTCCCAATCTTAACTTTGGTGGTGGAGAGATGTCCTCAACAGGAGC	1123
QY	933	TGATGACAGCAATGGGATTTGGTTATGTTAAATGCGCAGCAATACCTGTCCAAAGCCTG	992
Db	1124	TGATGACAGCAATGGGATTTGGTTATGTTAAATGCGCAGCAATACCTGTCCAAAGCCTG	1183
QY	993	ACTTTATCCCGAGTCTCATTTCTGCTGGTGGCTGTAATGACAGCTTTGTGAGNAAA	1052
Db	1184	ACTTTATCCCGAGTCTCATTTCTGCTGGTGGCTGTAATGACAGCTTTGTGAGNAAA	1243
QY	1053	TTTTGCGGTGGTGGACAAATCAGTAGATTTCAATGAGAAAGCAAAAGCCTCCAAATGGAT	1112
Db	1244	TTTTGCGGTGGTGGACAAATCAGTAGATTTCAATGAGAAAGCAAAAGCCTCCAAATGGAT	1303
QY	1113	GTGTTCTAGTCACTGTTTAGCTGGGATCTCCCGTCCGCCACCAATCGCTATGCGCTTACA	1172
Db	1304	GTGTTCTAGTCACTGTTTAGCTGGGATCTCCCGTCCGCCACCAATCGCTATGCGCTTACA	1363
QY	1173	TCATGAAGAGGATGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAGAC	1232
Db	1364	TCATGAAGAGGATGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAGAC	1423
QY	1233	CTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAAGATTA	1292
Db	1424	CTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAAGATTA	1483
QY	1293	AGAACAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGC	1352
Db	1484	AGAACAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGC	1543
QY	1353	CAAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAGGGAGAGCGCCCTCAGTC	1412
Db	1544	CAAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAGGGAGAGCGCCCTCAGTC	1603
QY	1413	CACCTGTGCGCACTCTGCTACTCAGAGGCGAGGACAAAGGCCCGTGTGATCCCGCCA	1472
Db	1604	CACCTGTGCGCACTCTGCTACTCAGAGGCGAGGACAAAGGCCCGTGTGATCCCGCCA	1663
QY	1473	GGGTGCCAGCGTGGCCAGCGTGCAGCCGTCTGCTGTAGAGGACAGCGCCGTGTACAGG	1532
Db	1664	GGGTGCCAGCGTGGCCAGCGTGCAGCCGTCTGCTGTGTAGAGGACAGCGCCGTGTACAGG	1723
QY	1533	CGGTACGTGGGTGCACTGTGCGGACAGAGCGCTGGAAAGACAGCAATAGCTCAAGCGTT	1592
Db	1724	CGGTACGTGGGTGCACTGTGCGGACAGAGCGCTGGAAAGACAGCAATAGCTCAAGCGTT	1783
QY	1593	CCTTCTCTGAGATCAAACTCAGTTTCAATTTCAAGCCAGCATGCGCAGCATCTTACATG	1652
Db	1784	CCTTCTCTGAGATCAAACTCAGTTTCAATTTCAAGCCAGCATGCGCAGCATCTTACATG	1843
QY	1653	GCTTCTCTCATCAGAGATGCTTTTGGAAATACATAAAACCTTCCACTACTCTGGATGGGA	1712
Db	1844	GCTTCTCTCATCAGAGATGCTTTTGGAAATACATAAAACCTTCCACTACTCTGGATGGGA	1903
QY	1713	CCAAACAAGCTATCCAGTCTCTCCCTGTTTTCAGGAATATCGGAGCAGACTCCCGAAACCA	1772
Db	1904	CCAAACAAGCTATCCAGTCTCTCCCTGTTTTCAGGAATATCGGAGCAGACTCCCGAAACCA	1963
QY	1773	GTCTGTATAAGGAGGAGCCAGCATCCCAAGAGCTGCGAGCCGCGCAGGCTTCAGACA	1832
Db	1964	GTCTGTATAAGGAGGAGCCAGCATCCCAAGAGCTGCGAGCCGCGCAGGCTTCAGACA	2023
QY	1833	GCCAGAGCAAGCGATTGCAATTCGCTCAGAACCAACAGCAGTGGCAACCGCCAGAGTCCC	1892
Db	2024	GCCAGAGCAAGCGATTGCAATTCGCTCAGAACCAACAGCAGTGGCAACCGCCAGAGTCCC	2083
QY	1893	TTTTATCTCCACTGCAATGAAAGTGGGAGCGTGGAGCAATTAACACACAGGCTTCTTT	1952
Db	2084	TTTTATCTCCACTGCAATGAAAGTGGGAGCGTGGAGCAATTAACACACAGGCTTCTTT	2143
QY	1953	TCGGCCTTTCCACAGCCAGCAGCACCTCAACGAAGTCTGCTGGCCTGGGCTTTAAGGGCT	2012
Db	2144	TCGGCCTTTCCACAGCCAGCAGCACCTCAACGAAGTCTGCTGGCCTGGGCTTTAAGGGCT	2203
QY	2013	GGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGTGATTT	2072
Db	2204	GGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGTGATTT	2263
QY	2073	TTGCCACAGAGTCTCTACACTTCTACTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT	2132
Db	2264	TTGCCACAGAGTCTCTACACTTCTACTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT	2323
QY	2133	ACTTGGCTTACAGCTGAGCGAGCTGCCCACTGCGGAGACCAAGTCTATTTCTGCGGCA	2192
Db	2324	ACTTGGCTTACAGCTGAGCGAGCTGCCCACTGCGGAGACCAAGTCTATTTCTGCGGCA	2383
QY	2193	GGCGGCAAGCCCAAGTGCAGAGCTGACCTCGCGGGGAGCTGGCATGAAGAGAGCCCT	2252
Db	2384	GGCGGCAAGCCCAAGTGCAGAGCTGACCTCGCGGGGAGCTGGCATGAAGAGAGCCCT	2443
QY	2253	TTGAAAAGCAGTTTAAACGCGAAGCTGCCAAATGGAAATTTGGAGAGAGCATCATGTGAG	2312
Db	2444	TTGAAAAGCAGTTTAAACGCGAAGCTGCCAAATGGAAATTTGGAGAGAGCATCATGTGAG	2503
QY	2313	AGAACAGCTCAGCGAAGAGCTGGGAAAGTGGGCGAGTCACTGCTAGCTTTTCGGGAGCA	2372
Db	2504	AGAACAGCTCAGCGAAGAGCTGGGAAAGTGGGCGAGTCACTGCTAGCTTTTCGGGAGCA	2563
QY	2373	TGGAATCAATTTGAGGTCTCTGTGAGAGAAAGACACTTTGTGACTTCTATAGACAATTTTT	2432
Db	2564	TGGAATCAATTTGAGGTCTCTGTGAGAGAAAGACACTTTGTGACTTCTATAGACAATTTTT	2623
QY	2433	TTTCTTGTTCACAAAATAATTCCTGTAAATCTGAAATATATATATATATATATATATAT	2492
Db	2624	TTTCTTGTTCACAAAATAATTCCTGTAAATCTGAAATATATATATATATATATATATAT	2683
QY	2493	ATTTTGTGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC	2552
Db	2684	ATTTTGTGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGATCAACCCAGTTGTTACTC	2743
QY	2553	TCCTTAACATCTGCATTTTGGAGATCAGCTAATCTTCTCTCAACAAAATAATGGAAGGCGAG	2612
Db	2744	TCCTTAACATCTGCATTTTGGAGATCAGCTAATCTTCTCTCAACAAAATAATGGAAGGCGAG	2803
QY	2613	ATGCTAGAAATCCCCCTAGACGGAGGAAACCAATTTTATTCAGTGAATTAACATCTCTCT	2672
Db	2804	ATGCTAGAAATCCCCCTAGACGGAGGAAACCAATTTTATTCAGTGAATTAACATCTCTCT	2863
QY	2673	TGTTCTTAAAAAGCAAGTGTCTTTTGGTGTGGAGGACAAAATCCCTTACATTTTCCAC	2732
Db	2864	TGTTCTTAAAAAGCAAGTGTCTTTTGGTGTGGAGGACAAAATCCCTTACATTTT-CAC	2922
QY	2733	GTGTGCTACTAAGAGATCTCAAAATATAGTCTTTGTCCGGAGCCCTTCCATAGTACACCT	2792

Db	2923		GTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCGGACCCCTTCCATAGTACACCT	2982
Qy	2793		TAGCGCTCAGACTGAGCCAGCTTTGGGGGTCAAGTAGTAGACCCCTGTTTAGGGACAGAGCC	2852
Db	2983		TAGCGCTCAGACTGAGCCAGCTTTGGGGGTCAAGTAGTAGACCCCTGTTTAGGGACAGAGCC	3042
Qy	2853		TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC	2912
Db	3043		TAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTCACC	3102
Qy	2913		TCACAGCCGAGGGACAGAGCATCACTCTGCTGGACGGACCACTTAGGGGCCCTGCCAAGG	2972
Db	3103		TGACAGCCGAGGGACAGAGCATCACTCTGCTGGACGGACCACTTAGGGGCCCTGCCAAGG	3162
Qy	2973		TCCTACITTAGAGCAAAACCCAGTAGCTCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT	3032
Db	3163		TCCTACITTAGAGCAAAACCCAGTAGCTCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT	3222
Qy	3033		ATCTCGTAGGCCATTTTCTTAGGCATTGTGAAATAGGTAGGTAGTACGTAGTCACACTTTTCAGA	3092
Db	3223		ATCTCGTAGGCCATTTTCTTAGGCATTGTGAAATAGGTAGGTAGTACGTAGTCACACTTTTCAGA	3282
Qy	3093		CCAAATTCAAACTGTCTATGCACAAAATTCOCGTGGGCCCTAGATGGAGATAATTTTTTTTT	3152
Db	3283		CCAAATTCAAACTGTCTATGCACAAAATTCOCGTGGGCCCTAGATGGAGATAATTTTTTTTT	3342
Qy	3153		CTTCTCAGCTTTATGAAGAGAGGGGAACTGTCTAGGATTCAGCTGACCAACCAAGGAACC	3212
Db	3343		CTTCTCAGCTTTATGAAGAGAGGGGAACTGTCTAGGATTCAGCTGAAACCAACCAAGGAACC	3402
Qy	3213		TGGCAACATCAGATTTAAAGCTAAGGTTGGGAGGCTTAAACGAGTCTACCTCCCTCTTTGTA	3272
Db	3403		TGGCAACATCAGATTTAAAGCTAAGGTTGGGAGGCTTAAACGAGTCTACCTCCCTCTTTGTA	3462
Qy	3273		AATCAAGAATTGTTTAAATGGGAATGTGCATTCCTTTTAAATAAAGATGAACCTTGGTTTC	3332
Db	3463		AATCAAGAATTGTTTAAATGGGAATGTGCATTCCTTTTAAATAAAGATGAACCTTGGTTTC	3522

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 27, 2004, 19:06:08 ; Search time 587 Seconds

(without alignments)
3741.599 Million cell updates/sec

Title: US-09-964-277-21

Perfect score: 517

Sequence: 1 MLPISLQVFLYFWNRR.....LKGVSQSSFGSWEIIEVS 517

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6745146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q/cn2_1/USPTO.spool/US09964277/runat 25022004 085401 2201/app query.fasta.1.711
-DB=N_Geneseq 25Jan04 -QMT=fascap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
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-USER=US09964277 @CGN 1 1 470 @runat 25022004 085401 2201 -NCFU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq 29Jan04.*

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- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002s.*
- 7: Geneseq2003as.*
- 8: Geneseq2003bs.*
- 9: Geneseq2003cs.*
- 10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	100.0	3332	6	ABK48378 cDNA enco
2	488	94.4	2102	7	ADA53105 Human cod
3	488	94.4	2732	4	AD09492 Human SGP
4	488	94.4	2966	4	AH99685 Human pro
5	488	94.4	3059	6	AAS15768 cDNA sequ
6	488	94.4	3104	6	ABN59704 Novel hum
7	488	94.4	3496	6	ABK47596 cDNA enco
8	488	94.4	3544	5	AAS14639 Human cDN

9	488	94.4	3544	6	ABK49402	Abk49402 cDNA enco
10	488	94.4	3766	6	ABK14474	Abk14474 Human pro
11	488	94.4	4790	6	ABN83966	Abn83966 Human gen
12	488	94.4	5145	5	ABV20833	Abv20833 Human pro
13	488	94.4	5145	5	ABV21080	Abv21080 Human pro
14	488	94.4	5145	5	ABV26680	Abv26680 Human pro
15	488	94.4	5145	5	ABV20978	Abv20978 Human pro
16	488	94.4	5145	5	ABV21092	Abv21092 Human pro
17	488	94.4	5145	5	ABV21312	Abv21312 Human pro
18	488	94.4	5145	5	ABV21316	Abv21316 Human pro
19	488	94.4	5145	5	ABV26826	Abv26826 Human pro
20	488	94.4	5145	5	ABV27131	Abv27131 Human pro
21	488	94.4	5145	5	ABV26923	Abv26923 Human pro
22	488	94.4	5145	5	ABV27135	Abv27135 Human pro
23	488	94.4	5145	5	ABV28657	Abv28657 Human pro
24	488	94.4	5145	5	ABV22827	Abv22827 Human pro
25	488	94.4	5145	5	ABV26934	Abv26934 Human pro
26	472	91.3	5450	6	ACC60559	Acc60559 Polynucle
27	472	91.3	5450	6	ACC60572	Acc60572 Polynucle
28	455	88.0	2118	4	RAF30479	Raf30479 Human pro
29	350	67.7	5111	6	ACC60521	Acc60521 Polynucle
30	138	26.7	425	5	ABV10726	Abv10726 Human pro
31	137	26.5	467	5	ABV40998	Abv40998 Human pro
32	137	26.5	467	5	ABV31891	Abv31891 Human pro
33	133	26.5	467	5	ABV40849	Abv40849 Human pro
34	133	25.7	408	5	ABV10907	Abv10907 Human pro
35	132	25.5	438	5	ABV32059	Abv32059 Human pro
36	67	13.0	355	5	ABV01738	Abv01738 Human pro
37	63	12.2	2756	6	ACC60560	Acc60560 Polynucle
38	58	11.2	411	5	ABV01557	Abv01557 Human pro
39	50	9.7	301	4	AAK53879	Aak53879 Murine tr
40	45	8.7	749	4	AAH06539	Aah06539 Human cDN
41	42	8.1	345	5	ABV02076	Abv02076 Human pro
42	42	8.1	346	5	ABV11245	Abv11245 Human pro
43	42	8.1	377	5	ABV41320	Abv41320 Human pro
44	42	8.1	377	5	ABV32391	Abv32391 Human pro
45	36	7.0	419	5	ABV32042	Abv32042 Human pro

ALIGNMENTS

RESULT 1

ABK48378
ID ABK48378 standard; cDNA; 3332 BP.

AC ABK48378;

DT 02-JUL-2002 (first entry)

DE cDNA encoding human DSP-16 alternative form protein.

XX Human; dual-specificity phosphatase-3; DSP-16; autoimmune disease;
KW mitogen-activated protein kinase; MAP; Duchenne muscular dystrophy;
KW cancer; graft-versus-host disease; allergy; metabolic disease;
KW abnormal cell growth; abnormal cell proliferation; contact inhibition;
KW cell cycle abnormality; anchorage independent cell growth; apoptosis;
KW intercellular adhesion; DSP-16 modulator; chromosome 12p; gene; ss.

XX Homo sapiens.

XX Location/Qualifiers

FT Key

FT CDS

FT FT
FT FT
FT FT
FT FT

WO200226997-A2.

04-APR-2002.

25-SEP-2001; 2001WO-US030124.

26-SEP-2000; 2000US-0235487P.

RESULT 2

ADA53105
 ID ADAS3105 standard; cDNA; 2102 BP.
 XX
 AC ADA53105;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human coding sequence, SEQ ID 673.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
 XX
 DR WPI; 2003-395539/38.
 DR P-PSDB; ADA54744.
 XX
 XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 1; SEQ ID NO 673; 205pp; English.
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX
 SQ Sequence 2102 BP; 542 A; 546 C; 510 G; 504 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 2102
 Score: 488.00 Matches: 488
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.39% Indels: 0
 DB: 7 Gaps: 0
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 QY 30 GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
 DB 587 GAGCTGATGCAGCAAGATGGGATGGTTATGTTTAAATGCCAGCAATACCTGTCCAAAG 646
 QY 50 ProAspPheIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
 DB 647 CCTGACTTTATCCCGAGTCTCAATTCCTGGGTGGCTGTGTGATGACAGCTTTGTGAG 706
 QY 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
 DB 707 AAAATTTTCCCGTGTGGCAAAATCAGTAGATTTCATTGGAAAGCAAAAGCTCCAAAT 766
 QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109

DB 767 GGATGTGTTCTAGTGACATGTTTAGTGGGATCTCCGCTCCGCCACCATCGTATCGCC 826
 QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
 DB 827 TACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTTGTGAAGAAAAA 886
 QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
 DB 887 AGACCTACTATATCTCAAACTTCATTTCTGGGCCAACTCTGGACTATGAGAAGAG 946
 QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu 169
 DB 947 ATTAAGAACCAAGCTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACTGGAG 1006
 QY 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
 DB 1007 AAGCCAAATGAACCTGTCCCTGTCTCAGAGGGTGGACAGAAAGCCAGAGCCCTTC 1066
 QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
 DB 1067 AGTCCACCTGTGCCGACTCTGCTACTCAGAGGACAGGACMAAGGCCGTGCTATCCC 1126
 QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
 DB 1127 GCCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGT 1186
 QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLys 249
 DB 1187 CAGCGCTCAGTGGCTGCACCTGTCCGACAGACAGGCTGGAAGACAGCAATTAAGCTCAAG 1246
 QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
 DB 1247 CGTTCTCTCTCTGGATATCAAACTCAGTTTCATATTCAGCCAGCATGCGCATCCTTTA 1306
 QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
 DB 1307 CATGGCTTCTCTCATCAGAAAGATGCTTGGAAATATACAAACCTTCCACTACTCTGGAT 1366
 QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
 DB 1367 GGGACCAACAAGCTATGCCAGTTCTCCCTGTTCAGAACTATCGGAGCAGACTCCCGAA 1426
 QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
 DB 1427 ACCAGTCTCATAGGAGGAGGAGCCAGCATCCCCAAGAGCTGCGAGCTGCCAGGCCCTTCA 1486
 QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
 DB 1487 GACAGCCAGAGCAAGCGATTTGCATTGGTCAAGAACCCAGCAGCAGTGGCACCCGCCAGAGG 1546
 QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
 DB 1547 TCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGAGGACAAATACCACACACAGCTTC 1606
 QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLys 389
 DB 1607 CTTTTCGGCTTTCCACAGCCAGCAGCAGCCTCACGAGTCTGCTGGCCTGGGCTTAAG 1666
 QY 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
 DB 1667 GCGTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTCCAGCAGCAGCTGG 1726
 QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
 DB 1727 TATTTGGCAGAGTCTCTACACTTCTACTCTGCCTCAGCCATCTACGGAGGAGCAGTGCC 1786
 QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
 DB 1787 AGTTACTCTGCTACAGCTGACGAGCAGCTGCCACTTGGGAGACCAAGTCTATCTCTGTC 1846
 QY 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgSerTrpHisGluGluSer 469

Db 1847 CGCAGCGGCGAAGCCAAAGTCACAGAGCTGACTCGCGGGAGCTGGCATGAGAGAGC 1906
 QY 470 ProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
 Db 1907 CCCTTTGAAAGACGTTTAAACGCGAAGAGCTGCCAAATGGAATTTGGAGAGACATCATG 1966
 QY 490 SerGluAsnArgSerArgGluGluLeuGlyValGlySerGlnSerSerPheSerGly 509
 Db 1967 TCAGAGACAGCTCAGCGGAGAGCTGGGAAAGTGGGAGTGGGAGTCACTAGCTTTTCGGGC 2026
 QY 510 SerMetGluIleGluValSer 517
 Db 2027 AGCATGGAATCATTTAGGTCTCC 2050
 RESULT 3
 AAD09492
 ID AAD09492 standard; DNA; 2732 BP.
 XX
 AC AAD09492;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human SGP002 phosphatase polypeptide encoding DNA.
 XX
 KW Human; SGP002 phosphatase polypeptide, phosphatase-related disease;
 KW immune-related disorder; ocular disease; organ transplant rejection;
 KW infection; diabetes; pain; sexual dysfunction; Alzheimer's disease;
 KW metabolic disorder; haematopoietic cancer; mood disorder; cardiac;
 KW Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis;
 KW cardiovascular disease; brain; neuronal-associated disease; dyskinesia;
 KW attention disorder; cognition disorder; psychotic disorder; cytostratic;
 KW neurological disorder; virucide; nootropic; cerebroprotective; therapy;
 KW neuroprotective; antibacterial; vulnary; tranquilliser; antiasthmatic;
 KW hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive;
 KW antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase;
 KW MKP; migraine; chromosome 12p11.1-p12.1; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 538..2535
 FT /tag= a
 FT /product= "Human SGP002 phosphatase polypeptide"
 XX
 PN WO200146394-A2.
 XX
 XX 28-JUN-2001.
 XX
 XX 21-DEC-2000; 2000WO-US034736.
 XX
 XX 21-DEC-1999; 99US-0173255P.
 XX
 XX 28-DEC-1999; 99US-0175766P.
 XX
 XX 25-JAN-2000; 2000US-0178078P.
 XX
 XX 31-JAN-2000; 2000US-0179301P.
 XX
 XX (SUGEN-) SUGEN INC.
 XX
 XX Plowman GD, Martinez R, Whyte D, Manning G, Sudareanam S;
 XX Hill RJ, Flanagan P;
 XX WPI; 2001-418058/44.
 XX P-PSDB; AAE04834.
 XX
 XX Novel phosphatase polypeptide useful for treating cancers, immune-related
 XX diseases and disorders, cardiovascular disease, brain or neuronal-
 XX associated diseases and metabolic disorders.
 XX
 XX Claim 29; Fig 1; 186pp; English.
 XX
 XX The present invention relates to phosphatase polypeptides, nucleotide
 XX sequences encoding them, as well as various products and methods useful
 XX for the diagnosis and treatment of various phosphatase-related diseases
 XX and conditions. Substance that modulates the activity of phosphatase

CC polypeptide is used to treat immune-related diseases and disorders,
 CC cardiovascular disease, brain or neuronal-associated diseases and
 CC metabolic disorders, including cancers of tissues, cancers of
 CC haematopoietic origin, diseases of central and peripheral nervous system,
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic
 CC lateral sclerosis, viral infections, infections caused by prions,
 CC bacteria and fungi, ocular diseases, diabetes, migraines, pain, sexual
 CC dysfunction, mood disorders, attention disorders, neurological disorders,
 CC dyskinesia, hypertension, psychotic disorders, neurodegenerative disorders,
 CC encoding human SGP002 phosphatase polypeptide. This sequence is a DNA
 CC classified as dual specificity phosphatase (DSP) and MAP kinase
 CC phosphatase (MKP). SGP002 gene maps to chromosomal position 12p11.1-p12.1
 XX
 XX Sequence 2732 BP; 710 A; 684 C; 686 G; 652 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 2732
 Score: 488.00 Matches: 488
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.39% Indels: 0
 DB: 4 Gaps: 0
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 QY 30 GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
 Db 1069 GAGCTGATGCGACAGAAATGGGATTTGGTATGTATTAATCCAGCAATACCTGTCCAAAG 1128
 QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
 Db 1129 CTTGACTTTATCCCGAGTCTCATTTCTCGGTGGCTGTGATGACAGCTTTTGTGAG 1188
 QY 70 LysIleLeuProTyrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
 Db 1189 AAAATTTTGGCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAGCTCCCAAT 1248
 QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
 Db 1249 GGATGTGTCTAGTGCACATGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGTATCGCC 1308
 QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
 Db 1309 TACATCATGAAGAGGATGGACATCTCTTTAGTAGAAGCTTACAGATTGTGAAAGAAAA 1368
 QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyClnLeuLeuAspTyrGluLysLys 149
 Db 1369 AGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCCACTCTCTGGACTATGAGAGAG 1428
 QY 150 IleLysAsnGlnThrGlyValAsnGlyProLysSerLysLysLeuLysLeuHisLeuGlu 169
 Db 1429 ATTAGAACACAGACTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTGTGACCTGGAG 1488
 QY 170 LysProAsnGluProValProAlaValSerGluClyGlyGlnLysSerGluThrProLeu 199
 Db 1489 AAGCCAAATGAACCTGTCTCTCTGCTGTCTCAGAGGTGGACAGAAAGCGAGCGCCCTC 1548
 QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
 Db 1549 AGTCACCTCTGTGCCACTCTGCTACTCAGAGCAGCAGGACAAAGCCCGCTGCATCCC 1608
 QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
 Db 1609 GCCAGCTGTGCCAGCGTCCCGAGCGTGCAGCGCTGCTGTGTAGAGGACAGCGCCCTGTA 1668
 QY 230 GlnAlaLeuSerGlyLeuHisSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
 Db 1669 CAGCGCTCTCAGTGGGCTGCACCTGTCTCCGACAGAGCTGGAGACACATATAGCTCAAG 1728
 QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
 Db 1729 CATTCTCTCTCTGATATCAATCAATCAATTCATATTATTCAGCCAGCATGGCAGCATCTTA 1788

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QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrIysProSerThrThrLeuAsp 289
Db 1789 CATGGCTTCTCTCATCAGAGATGCTTGGAACTACTACAACTTCCACTACTCTGGAT 1848
QY 290 GlyThrAsnLysLeuCyAGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1849 GGGACCAACAGCTATGCGAGTCTCCCTCTGTTCCAGACTATCCGAGCAGATCCCGAA 1908
QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaA-gProSer 329
Db 1909 ACCAGTCTCTGATAGAGGAGGAGCAGCATCCCCAGAGAGCTGCAGACTGCCAGCCCTTCA 1968
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
Db 1969 GACACCCAGAGCAACGAGTTCATTCGTCAGAACCCAGAGCAGTGCAGACTGCCAGCCCTTAAG 2028
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 2029 TCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGACATTAACACACAGCTTC 2088
QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 2089 CTTTTCGGCCTTTCACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2148
QY 390 GlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyr 409
Db 2149 GGCCTGGCACTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACACAGCAGCTGG 2208
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlySerAla 429
Db 2209 TATTTTGGCACAGAGTCTCTCACTTCTACTCTGCTCAGCCATCTACGGAGGAGCAGTGC 2268
QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2269 AGTTACTTTCCTCAGCTCAGCTCAGCCAGCTGCCCTTCTCGGAGACCAAGTCTATTCGTG 2328
QY 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgSerTrpHisGluGluSer 469
Db 2329 CGCAGCGCGCAGAACCCAAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAGAGAGC 2388
QY 470 ProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2389 CCCTTTGAAAGACATTTAAACGCGAGAGCTGCCAAATGGAAATTTGAGAGAGCATCATG 2448
QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2449 TCAGAGACAGCTCAGCGGAGAGCTGGGAAAGTGGGCACTGAGTCTAGCTTTTCGGGC 2508
QY 510 SerMetGluIleLeuGluValSer 517
Db 2509 AGCATGGAATCATTTGAGGTCTCC 2532
```

RESULT 4

AAH99685

ID AAH99685 standard; cDNA; 2966 BP.

XX

AC AAH99685;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein encoding cDNA sequence SEQ ID NO:520.

XX

Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antibacterial; antirheumatic; antidiabetic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
antiaggregant; haemostatic; vulnary; antidiabetic; eczema;
dermatological; antiallergic; antidiabetic; antidiabetic; cytostatic;
neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

genetic disease; haematopoietic disorder; platelet disorder; asthma;
thrombocytopenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
neurological disorder; ss.
XX Homo sapiens.
XX WO200153455-A2.
XX 26-JUL-2001.
XX 22-DEC-2000; 2000WO-US035017.
XX 23-DEC-1998; 89US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457603/49.
XX P-PSDB; AAM25744.
XX Isolated human polynucleotides encoding polypeptides, useful for the
treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX Claim 1; Page 578; 1217pp; English.
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
AAM25963. The proteins can have activities based on the tissues and cells
they are expressed in, such as: antiinflammatory; antirheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
central nervous system; virucide; anti-HIV; fungicide; antimutagen;
cardiovascular; antianemic; antiaggregant; haemostatic; vulnary;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antiparkinsonian; and immunostimulant. The proteins and polynucleotides
encoding them can be used in gene therapy, antisense therapy and vaccine
production. The proteins and polynucleotides are useful for screening for
agonists or antagonists of a protein and for the treatment and diagnosis
of disorders associated with the activity of a protein e.g. inflammation,
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
infections, autoimmunity, genetic diseases, haematopoietic disorders,
anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
osteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
Alzheimer's disease, Parkinson's disease, neurodegenerative and
neurological disorders

XX Sequence 2966 BP; 809 A; 735 C; 688 G; 733 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	0	Length:	2966
Score:	488.00	Matches:	488
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.39%	Indels:	0
DB:	4	Gaps:	0

US-09-964-277-21 (1-517) x AAH99685 (1-2966)

QY 30 GluLeuMetGlnGlnAsnGlyLeGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
Db 554 GAGCTGATGACGAGATGGGATGGTATGTGTAAATCCAGCAATACCTGTCCAAAG 613
QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 614 CTGACTTATCCCGAGTCTCATTTCTCGGTGCTGCTGATGACACTTTTGAG 673
QY 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89

Db 674 AAATTTTCCCGTGGTGGACAAATCAGTAGAATTCATTGGAAGCAAAAGCCCTCCAAT 733
Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 734 GGATGTGTTCTAGTGCACATGTTAGTGGATCTCCCGCTCCGCCACCATCGCTATCGCC 793
Qy 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 794 TAGCATGAAGAGGATGACATGCTTTAGATGAAGCTTACAGATTGTGTAAGAAAAA 853
Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 854 AGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTTGACTATGAGAAGAAG 913
Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
Db 914 ATTAAAGAACCCAGACTGGACATCAGGGCCAAAGACCAACTCAAGCTCTGCACCTGGAG 973
Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
Db 974 AAGCCAAATGAACCTGCTCCTGCTGCTCAGAGGGTGGACAGAAAGCGAGCGCCCTC 1033
Qy 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
Db 1034 AGTCCACCCCTGTCCGACTCTGTACTCTCAGAGGGCAGCAGCAAAAGCCCGTGCATCC 1093
Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1094 GCCAGCGTGGCCAGGTGCCAGCGTGCAGCGTGCCTGCTTTAGAGCAGCGCCGCTGGTA 1153
Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1154 CAGCGCGTCACTGAGTGGCTGACCTGTCCGAGCAGCGCTGGAAGACAGCAATAAGCTCAAG 1213
Qy 250 ArgSerPheSerLeuAspLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
Db 1214 CGTTCCTCTCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGTCCCTTA 1273
Qy 270 HisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1274 CATGGCTTCTCTCTCATCAGAGATGCTTTGGAACTACTACAAACCTTCCACTACTCGAT 1333
Qy 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1334 GGGACCAACAAAGCTATGCCAGTTCTCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAA 1393
Qy 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1394 ACCAGTCTGATAGGAGGAGCAGCAGCATCCCCAGAGCTGCAGACCGCCAGGCTTCA 1453
Qy 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
Db 1454 GACAGCCAGAGCAAGCATTCGATTCGCTCAGAACCCAGCAGCAGTGGCACCAGCCAGGAG 1513
Qy 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 1514 TCCCTTTTATCTCCACTGCATCGAAGTGGAGGCGTGGAGGCAATTACACACCCAGCTTC 1573
Qy 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 1574 CTTTTTCGGCTTTCACACCCAGCAGCAGCTCAACGAGTCTGCTGGCTGGCTTAAAG 1633
Qy 390 GlyThrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
Db 1634 GGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCCAGCAGCTGG 1693
Qy 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlySerAla 429
Db 1694 TATTTTGGCCACAGAGTCTCTCAGCTTCTACTCTGCTCTAGCCATCTACGGAGGAGTGGC 1753
Qy 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449

Db 1754 AGTACTCTGCTACAGCTGCAGCCAGCTGCCACTTTCGGAGACCAAGTCTATTCTGTG 1813
Qy 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgSerTrpHisGluGluSer 469
Db 1814 CGCAGCGCGCAGAAAGCCAAAGTGACAGAGCTGACTCGCGCGGAGCTGCCATGAAGAGC 1873
Qy 470 ProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 1874 CCCTTTGAAAGCAGCTTTAAACGCGAAGCTGCCAAATGGAAATTTGGAGAGACATCATG 1933
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 1934 TCAGAGAAACAGCTCACGGGAAAGAGCTGGGAAAGTGGCGACAGTCTAGCTTTTCGGGC 1993
Qy 510 SerMetGluIleIleGluValSer 517
Db 1994 AGCATGGAATCATTTAGGTCTCC 2017
RESULT 5
AAS15768
ID AAS15768 standard; cDNA; 3059 BP.
XX
XX AAS15768;
AC
XX
DT 18-JUN-2002 (first entry)
XX
DE cDNA sequence of human (dual specificity phosphatase) DUSP-10.
XX
KW Human; dual specificity phosphatase; DUSP-10; cancer; epilepsy; stroke;
KW neuronal degeneration syndrome; Alzheimer's disease; depression;
KW schizophrenia; asthma; immune disorder; inflammatory process; arthritis;
KW osteoporosis; diabetes; gene therapy; chromosome 12; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 127..2124
FT /*tag= a
FT /product= "DUSP-10 protein"
XX
XX WO200177340-A1.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-EF003966.
XX
XX 10-APR-2000; 2000EP-00107143.
XX
XX (MERE) MERCK PATENT GMBH.
XX
XX Duecker K;
XX
XX
XX WPI; 2002-010917/01.
XX P-PSDB; AAU09946.
XX
XX Novel dual specificity phosphatase polypeptides useful for treating
XX cancers, epilepsy, stroke, neuronal degeneration syndromes, Alzheimer's
XX disease, depression, schizophrenia, asthma and immune disorders.
XX
XX Claim 5; Page 34-37; 43pp; English.
XX
XX The present invention relates to a new isolated dual specificity
XX phosphatase (DUSP10) polypeptide, comprising a 665 residue amino acid
XX sequence that is fully defined in the specification. The invention also
XX provides a sequence encoded by a 3059 nucleotide sequence fully defined
XX in the specification, and a sequence having at least 95 % identity to the
XX polypeptide, or fragments or variants of DUSP-10. The invention is useful
XX for treating cancer e.g. leukaemia, colon carcinoma, lung cancer,
XX prostate cancer, metastasis of tumour cells, neo-angiogenesis, epilepsy,
XX stroke, neuronal degeneration syndromes, Alzheimer's disease, depression,
XX schizophrenia, cardiac myotrophies, asthma, immune disorders,
XX inflammatory processes e.g. arthritis, bowel disease, type I diabetes,
XX osteoporosis, diabetes and diabetes associated diseases. The molecules of

CC the invention are also useful as vaccines for inducing immunological
CC response in a mammal, in disease diagnosis and in assays for screening
CC agonistic or antagonistic compounds. Other uses of the invention include
CC identifying membrane bound or soluble receptors, as a diagnostic reagent,
CC in chromosome localisation studies, and as a valuable tool in tissue
CC expression studies. The present sequence represents cDNA of the human
CC dual specificity phosphatase, DUSP-10. DUSP-10 is located on chromosome
CC 12

XX Sequence 3059 BP; 831 A; 761 C; 709 G; 758 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3059
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 6 Gaps: 0

US-09-964-277-21 (1-517) x AAS15768 (1-3059)

QY 30 GluLeuMetGlnGlnAenGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
DB 658 GAGCTGATGAGCAGATGGATGGTATGTTAAATGCCAGCAATACCTGTCRAAG 717
QY 50 ProAspPheileProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
DB 718 CTTGACATTTATCCCGAGTCTCATTTCTTCGGTGTGCTGTGAATGACAGCTTTGTGAG 777
QY 70 LysileLeuProThrLeuAspLysSerValAspPheileGluLysAlaLysAlaSerAsn 89
DB 778 AAAATTTTGGCGTGGTGGCAATCATAGTAGATTTTCAATTGAGAAACCAAGCCCTCAAT 837
QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
DB 838 GGAATGTTTCTAGTGCACTGTTTACCTGGGATCTCCGCTCCGCCACCAATGCTATCGCC 897
QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
DB 898 TACATCATGAAGAGATGGACATCTCTTATAGTAGAGCTTACAGATTTGTGAAGAAAA 957
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrGluLysLys 149
DB 958 AGACCTACTATATCTCCAACTTCAATTTCTGGCCAACTCTCTGGACTATGAGAAGAG 1017
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu 169
DB 1018 ATTAAGAACCACTGGAGCATCAGGCCCAAGAGCAACTCAAGCTGTGCACCTGGAG 1077
QY 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
DB 1078 AAGCCAAATGAACCTGTCCCTGTCTCTCAGAGGGTGGACAGAAAAAGCAGAGCGCCCTC 1137
QY 190 SerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
DB 1138 AGTCCACCTGTGGCACTGTGCTACTCTCAGAGCAGCAGCAAAAGGCCGTGCAATCCC 1197
QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
DB 1198 GCCAGCGTCCCGAGCGTCCCGAGCGTGGCGTGTGTAGAGCAGACCGCGCTGGTA 1257
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuAspSerAsnLysLeuLys 249
DB 1258 CAGGCGCTCAGTGGGCTGCACCTGTCCGAGACAGGCTGGAAGACAGCAATAGCTCAAG 1317
QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
DB 1318 CGTTCCTTCTCTGGATATCAATCATAGTTTCAATTCAGCCAGCAGCATCCTTA 1377
QY 270 HisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
DB 1378 CATGGCTTCTCTCATCAGAAAGTGTCTTGGAAATACATAAACCCTTCCACTACTCTGGAT 1437

QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlnGlnThrProGlu 309
DB 1438 GGACCAAAAGCATATGACAGTTCCTCCCTGTTCAGGAACACTCGGAGCAGACTCCCCAA 1497
QY 310 ThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
DB 1498 ACCAGTCTCTGATAGGAGGAGCAGCATCCCAAGAGCTGCAGACCGCAGGCTTCA 1557
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
DB 1558 GACAGCCAGCAGCAAGCGATTGCTATCGGTCAAGACAGCAGCGTGGCACCCCGCAGAGG 1617
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
DB 1618 TCCCTTTTATCTCATCTGCATCGAGTGGAGCGTGGAGCAATATACACACAGCTTC 1677
QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
DB 1678 CTTTTCGGCCTTTCCACACGCCAGCAGCACCTCAGAAAGTCTGTGGCTGGGCTTAAG 1737
QY 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
DB 1738 GGTGGCACTCGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACACAGCAGCTGG 1797
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
DB 1798 TATTTTGGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGCAGTGC 1857
QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
DB 1858 AGTTACTTCTGCTTACAGCTGCAGCCAGCTGCCCACTTGGGAGACCAAGTCTATTCTGTG 1917
QY 450 ArgArgGlnLysProSerAspArgAlaAspSerArgSerTrpHisGluGluSer 469
DB 1918 CGCAGCGCGCAGAGCAAGTGCAGAGCTGACTCGCGCGAGCTGGCATGAAGAGAGC 1977
QY 470 ProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
DB 1978 CCCTTTGAAAGCAGTTTAAACGACAGAGCTGCCAAATGGAAATTTGGAGAGAGCATCATG 2037
QY 490 SerGluAsnArgSerArgGluLeuGluLysValGlySerGlnSerSerPheSerGly 509
DB 2038 TCAGAGNACAGCTCAGGGNAGAGCTGGGGAAGTGGGCAAGTGGCAGTCTTTTCGGGC 2097
QY 510 SerMetGluIleLeuGluValSer 517
DB 2098 AGCATGGAAATCATTTGAGTCTCC 2121
RESULT 6
ABNS9704
ID ABNS9704 standard; cDNA; 3104 BP.
XX AC ABNS9704;
XX DT 28-JUN-2002 (first entry)
XX DE Novel human coding sequence SEQ ID NO: 115.
XX KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;
XX KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
XX KW neuroprotective; antiparkinsonian; protein therapy; EST;
XX KW expressed sequence tag; gene; ss.
XX OS Homo sapiens.
XX PN WO200222660-A2.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US026015.
XX PR 11-SEP-2000; 2000US-00659671.
XX XX

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Weinman T, Drmanac RT;

XX WPI; 2002-292408/33.

DR P-PSDB; ABB97291.

XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.

PS Claim 1; SEQ ID NO 115; 509pp; English.

XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention

SQ Sequence 3104 BP; 845 A; 772 C; 718 G; 769 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3104
Score:	488.00	Matches:	488
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.39%	Indels:	0
DB:	6	Gaps:	0

US-09-964-277-21 (1-517) x AEN59704 (1-3104)

Qy	30	GLuLeuMetGlnGlnAsnGlyLeGlyTyrValLeuAsnAlaSerAsnThrCysProLys	49
Db	690	GAGCTGATGCAGCAGAAATGGGATGGTATGTTGTTAAATGCCAGCAATACCTGTCCAAAG	749
Qy	50	ProAspPheIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlu	69
Db	750	CTTGACTTTATCCCGAGTCTCATTTCTTCGCTGCGCTGGTGAATGACAGCTTTTGTGAG	809
Qy	70	LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn	89
Db	810	AAATTTTGGCGTGTGGACAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCTCCAAAT	869
Qy	90	GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla	109
Db	870	GGATGTGTCTAGTGACTGTTTAGCTGGGATCTCCGCTCCGCCACCATCGTATCGCC	929
Qy	110	TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys	129
Db	930	TACATCATGAAGAGGATGGACATGCTCTTTAGATGAAGCTTACAGATTGTGAAGAAAA	989
Qy	130	ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys	149
Db	990	AGACCTACTATATCTCCCACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAG	1049
Qy	150	IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu	169
Db	1050	ATTAGNACCAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTGCTGCACCTGGAG	1109
Qy	170	LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu	189
Db	1110	AAGCCAAATGAACCTGTCTGCTGTCTGATGAGGGTGGACAGAAAAAGGCAGACGCCCTC	1169
Qy	190	SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro	209
Db	1170	AGTCCACCTGTGCCGACTCTGTCTACTCAGAGGCAGCAGGCAAAAGGCCCTGTGATCCC	1229

Qy	210	AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal	229
Db	1230	GCACGGTGGCCAGCGTCCAGCGTCCAGCGTGGCTGTGTAGAGGACAGCCCGCTGGTA	1289
Qy	230	GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys	249
Db	1290	CAGGCGCTCAGTGGCTGCACCTGCCAGACAGGCTGGAAGACAGCAATAAGCTCAAG	1349
Qy	250	ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu	269
Db	1350	CGTCTCTCTCTGGATATCAATCAGTTTCATTCAGCCAGCATGGCAGCATCCTTA	1409
Qy	270	HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp	289
Db	1410	CATGCTCTCTCTCATCAGAAAGATGCTTTGGAATACATAAACCCTTCACTCTGGAT	1469
Qy	290	GlyThrAsnLysLeuCysGlnPheSerProValGlnGlnLeuSerGluGlnThrProGlu	309
Db	1470	GGGACCAACAGCTATGCCAGTTCTCCCTGTTCAGGAATATCGGAGCAGATCCCGAA	1529
Qy	310	ThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThrAlaAlaGProSer	329
Db	1530	ACCAGTCTGATAGGAGGAAGCCAGCATCCCAAGAGCTGCAGACCCGCGAGCTTCA	1589
Qy	330	AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg	349
Db	1590	GACAGCCAGAGCAAGCGATTGCTTCGTCAGAACCCAGCAGCATGGCCGCCAGG	1649
Qy	350	SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe	369
Db	1650	TCCCTTTTATCTCCACTGCATCGAAGTGGGAGCTGGAGCAATATACCAACAGGTTTC	1709
Qy	370	LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys	389
Db	1710	CTTTTCGGCTTTTCCACCAGCAGCACCTCAGAAAGTCTGCTGGCCTGGGCTTTAAG	1769
Qy	390	GlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTip	409
Db	1770	GGCTGGCACTGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGG	1829
Qy	410	TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla	429
Db	1830	TATTTTGCACAGAGTCTCTACACTTCTCTGCTCCTCAGCCATCTACGGAGGCAAGTGC	1889
Qy	430	SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal	449
Db	1890	AGTTACTCTGCCCTACAGCTGCAGCAGCTGCCACTTGGCGAGACCAAGTCTATTCTGTG	1949
Qy	450	ArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer	469
Db	1950	CGCAGCGCCAGAGCCAAAGTGACAGAGCTGACTCGCGCGGAGCTGCATGAAGAGAGC	2009
Qy	470	ProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet	489
Db	2010	CCCTTTGAAAAGCAGTTTAAACGCAGAGCTGCCAAATGGAAATTTGGAGAGAGCATCATG	2069
Qy	490	SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly	509
Db	2070	TGAGAGACAGCTACCGGAGAGAGCTGGGAAAGTGGCAGTCACTTAGCTTTTCGGGC	2129
Qy	510	SerMetGluIleIleGluValSer	517
Db	2130	AGCATGGAATCATTTAGGTCTCC	2153

RESULT 7

ABK47596
ID ABK47596 standard; cDNA; 3496 BP.XX
AC ABK47596;XX
DT 02-JUL-2002 (first entry)XX
DE cDNA encoding human dual-specificity phosphatase-3 (DSP-16) protein.

XX Human: dual-specificity phosphatase-3; DSP-16; autoimmune disease;
 KW mitogen-activated protein kinase; MAP; Duchenne muscular dystrophy;
 KW cancer; graft-versus-host disease; allergy; metabolic disease;
 KW abnormal cell growth; abnormal cell proliferation; contact inhibition;
 KW cell cycle abnormality; anchorage independent cell growth; apoptosis;
 KW intercellular adhesion; DSP-16 modulator; chromosome 12p; gene; ss.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT CDS 562..2559
 FT /tag= a
 FT /product= "Human dual-specificity phosphatase-3 (DSP-16)
 FT protein"
 XX
 PN WO200226997-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 25-SEP-2001; 2001WO-US030124.
 XX
 PR 26-SEP-2000; 2000US-0235487P.
 XX
 XX (CEPT-) CEPTYR INC.
 PA
 XX Luche RM, Wei B;
 PI
 FI WPI: 2002-315802/35.
 DR P-PSDB; ANU79156.
 XX
 XX New DSP-16 polypeptide, useful for identifying modulators of its
 PT activity, which can be used in the treatment of disorders such as
 PT Duchenne muscular dystrophy, or cancer.
 XX
 XX Claim 7; Fig 1; 97pp; English.
 PS
 XX The present invention relates to a new polypeptide, DSP-16, having a 665
 CC amino acid sequence, given in the specification, or a variant having at
 CC least 50 % identical residues, which retains the ability to
 CC dephosphorylate an activated mitogen-activated protein (MAP) kinase. The
 CC invention can be used for identifying agents which modulate DSP-16
 CC activity, for modulation of a proliferative response in a cell, survival
 CC of a cell, or differentiation of a cell. The cell displays contact
 CC inhibition of cell growth or anchorage independent growth and may display
 CC altered intercellular adhesion. The agent may modulate apoptosis, or the
 CC cell cycle. The identified modulators can be used to treat Duchenne
 CC muscular dystrophy, cancer, graft-versus-host disease, autoimmune
 CC diseases, allergies, metabolic diseases, abnormal cell growth, abnormal
 CC cell proliferation, and cell cycle abnormalities. The present nucleic
 CC acid sequence is that of the human dual-specificity phosphatase-3 (DSP-
 CC 16) gene located on chromosome 12p. This sequence encodes the human DSP-
 CC 16 protein of the invention
 XX
 SQ Sequence 3496 BP; 939 A; 854 C; 856 G; 847 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 3496
 Score: 488.00 Matches: 488
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.39% Indels: 0
 DB: 6 Gaps: 0
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 QY 30 GluLeuMetGlnGlnAsnGlyLeuValLeuAsnAlaSerAsnThrCysProLys 49
 DB 1093 GAGCTGATGCAGCAGATGGGATTGTTATGTTAAATGCCAGCAATACCTGTCCTCAAG 1152
 QY 50 ProAspPheLeuProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
 DB 1153 CCTGACATTTATCCCCGAGTCTCAATTCCTCGGTGCTGTGAATGACAGCTTTGTGAG 1212

QY 70 LysIleLeuProTrpIleuAspLysSerValAspPheIleGlyLysAlaLysAlaSerAsn 89
 DB 1213 AAAATTTTGGCGTGTGGCAAAATCAGTAGATTTTCATTGAGAAAGCAAAGGCTCCAAT 1272
 QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
 DB 1273 GGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC 1332
 QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
 DB 1333 TACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAA 1392
 QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
 DB 1393 AGACCTACTATATCTCCAACTTCATTTTCTGGGCCAACTCTCTGGACTATGAGAAGAG 1452
 QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu 169
 DB 1453 ATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTCACCTGGAG 1512
 QY 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
 DB 1513 AAGCAAATGAACTGTCTCTGCTCTCAGAGGGTGGACAGAAAGCAGAGAGCCCTTC 1572
 QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
 DB 1573 AGTCCACCTGTGCGGACTCTGCTACTCAGAGGCAGGAGCAAAAGGCCGCTGCATCCC 1632
 QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
 DB 1633 GCCAGCTGTCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGC 1692
 QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
 DB 1693 CAGCGCTCAGTGGCTGCGACCTGTCTCGCAGACAGCTGGAGACAGCAATAAGCTCAAG 1752
 QY 250 ArgSerPheSerLeuAspLysSerValSerValSerValSerAlaSerMetAlaAlaSerLeu 269
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 QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
 DB 1873 GGGACCAACAAGCTATGCCAGTTCTCCCTGTTCCAGAACTATCGAGCAGACTCCCGAA 1932
 QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
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 QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
 DB 1993 GACAGCCAGAGCAAGCGATTGCAATTCGGTCAAGACCAGCAGCAGTGGCACCCGCCAGAGG 2052
 QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
 DB 2053 TCCCTTTTATCTCCTCCTGATCAGAGTGGGAGCGTGGAGGACAATATACCAACACAGCTTC 2112
 QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
 DB 2113 CTTTTGGGCTTTTCCACCGCCAGCAGCAGCTTCAAGAGTCTGTGGCTTGGGCTTGAAG 2172
 QY 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
 DB 2173 GGCTGGCACTCGGATATCTTGGCCCCCAGAGCTCTACCCCTTCCCTGACCAACAGCTGG 2232
 QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
 DB 2233 TATTTTGGCCAGAGTCTCTCACTTCTTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 2292

Qy 430 SerTySerAlaTySerCysSerGlnLeuProThrCysGlyAspGlnValTySerVal 449
Db 2293 AGTTACTCTGCTACAGCTGCAGCCAGCTGCCACTTTCGGAGACCAAGTCTATCTGTG 2352
Qy 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgSerTrpHisGluGluSer 469
Db 2353 CCAGAGCGGACAGAGCCAGTACAGAGCTGACTCCGCGGAGCTGGCATGAAGAGAGC 2412
Qy 470 ProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2413 CCCTTTGAAAAGCAGTTTAAAGCGCAAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATG 2472
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2473 TCAGAAACAGGTCACGGAGAGAGCTGGGGAAGTGGGAGTCAAGTCTAGCTTTTCGGGC 2532
Qy 510 SerMetGluIleGluValSer 517
Db 2533 AGCATGGAAATCATTTGAGGTCTCC 2556
RESULT 8
AAS14639
ID AAS14639 standard; cDNA; 3544 BP.
XX
AC AAS14639;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding dual specificity phosphatase 21117.
XX
KW Human; ss; dual specificity phosphatase 21117; hepatotropic; cytostatic;
KW hematopoietic disorder; autoimmune disorder; diabetes mellitus;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW liver disorder; erythroid associated disorder; haemolytic anaemia;
KW cellular proliferative; differentiative disorder; leukaemia;
KW acute myeloid leukaemia; carcinoma; sarcoma; metastatic cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 589..2586
FT /tag= a
FT /product= "Dual specificity phosphatase 21117"
XX
PN WO200173059-A2.
XX
PD 04-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-US009477.
XX
PR 24-MAR-2000; 2000US-0191858P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PI Meyers RA;
XX
DR WPI; 2001-611635/70.
DR P-PSDB; AAU09016.
XX
PT New human dual specificity polypeptides and nucleic acids for diagnosis
PT of disease and treatment of e.g. liver disorders.
XX
PS Claim 1; Fig 1; 143pp; English.
XX
CC The invention relates to two novel human dual specificity phosphatases
CC designated 21117 and 38692, the nucleic acids encoding them (including
CC fragments, allelic variants, their complements or nucleic acids that
CC hybridize to them) and antibodies raised against the proteins. The
CC antibody is useful for detecting the presence of the polypeptide, and the
CC nucleic acid fragments are useful for detecting the presence of the
CC nucleic acid, for diagnosing disease. Agents (e.g. the antibody and
CC antisense sequences) are useful for modulating the activity or expression
CC of the polypeptide/nucleic acid, useful for the treatment of e.g.

CC hematopoietic disorders, autoimmune disorders (e.g. diabetes mellitus,
CC rheumatoid arthritis, multiple sclerosis, Crohn's disease and many others
CC listed in the specification) liver disorders, erythroid associated
CC disorders (e.g. haemolytic anaemia) cellular proliferative or
CC differentiative disorders, leukaemias (e.g. acute myeloid leukaemia),
CC carcinomas, sarcomas, metastatic cancers. Agents modulating 21117 and
CC 38692 are also useful for modulating the proliferation, survival, and
CC migration or differentiation of a 38692 or 21117-expressing cell. The
CC polypeptide and nucleic acids are useful for identifying modulating
CC agents. The present sequence encodes the dual specificity phosphatase
CC 21117
XX
SQ Sequence 3544 BP; 1000 A; 840 C; 822 G; 882 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 5 Gaps: 0
US-09-964-277-21 (1-517) x AAS14639 (1-3544)
Qy 30 GluLeuMetGlnGlnAsnGlyIleGlyTyTrValLeuAsnAlaSerAsnThrCysProLys 49
Db 1120 GAGCTGATGCAGCAGATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAG 1179
Qy 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 1180 CCGTACTTTATCCCGAGTCTCATTTCTCGGTGCTGCTGTAATGACAGCTTTTGGAG 1239
Qy 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
Db 1240 AAAATTTTCGCTGGTGGACAAATCAGTAGATTTCATTGGAAGCAAAAGCTCCAT 1299
Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 1300 GGATGTGTTCTAGTGCACGTGTTTAGCTGGGATCTCCCGCTCCGACCATCGTATCGCC 1359
Qy 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyArgPheValLysGluLys 129
Db 1360 TACATCATGAAGAGATGGACATGTCCTTTAGATGAGCTACAGATTGTGGAAGAAAA 1419
Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyTrGluLysLys 149
Db 1420 AGACCTACTATATCTCCAAACTTCAATTTCTGSGCCAACTCTCTGGACTATGAGAGAG 1479
Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuGlu 169
Db 1480 ATTAAAGAACCCAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTCTGCACCTGGAG 1539
Qy 170 LysProAsnGluProValProAlaValSerGlyGlyGlnLysSerGluThrProLeu 189
Db 1540 AAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGTGGACAGAAAGCGAGAGCCCTC 1599
Qy 190 SerProProCysAlaAspSerAlaThrSerGluAlaGlyGlnArgProValHisPro 209
Db 1600 AGTCACACCTGTGCGGACTCTGCTACCTCAGAGCAGCAGGCAAAAGCCCGTCATCCC 1659
Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1660 GCCAGCGTGCCCGGCTGCCAGCGTGCAGCCGCTGCTGTAGAGGACAGCCGCTGTA 1719
Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1720 CAGGCGCTCAGTGGCTGCACCTCTCCGACAGAGGTGGAGACAGCAATAAGCTCAAG 1779
Qy 250 ArgSerPheSerLeuAspIleLysSerValSerTyTrSerAlaSerMetAlaAlaSerLeu 269
Db 1780 CTTTCTCTCTCTGGAATATCAATTCAGTTTCATTTTCAGCCAGCATGGCAGCATCTT 1839
Qy 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyTrTyLysProSerThrThrLeuAsp 289

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Db 1840 CATGGCTTCTCTCATCAGAAAGTCCTTTGGAACTACAAACCTTCCACTACTCTGGAT 1899
QY GlyThrAsnLysLeuCysGlnPheSerProValGlnLeuSerGluGlnThrProGlu 309
Db 1900 GGGACCAACAAGCTATGCCAGTCTCTCCCTGTTCCAGGAACATATCGGAGCAGACTCCCGAA 1959
QY ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1960 ACCAGTCTGTATAGGAGAGAGCAGCATATCCCAAGAAAGCTGCAGACCCGACGCTTCA 2019
QY AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
Db 2020 GACAGCCAGAGCAAGCGATTGCATTTCGTAGAACACAGCAGCAGTGCACCGCCAGAGG 2079
QY SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 2080 TCCCTTTTATCTCCACTCATCGAAGTGGAGCGGTGGAGAGCAATACCAACACCGCTTC 2139
QY LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 2140 CTTTTCGGCTTTCACAGCCAGCAGCAGCACTCACGAAGTCTGCTGGCTGGGCTTAAG 2199
QY GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerTrp 409
Db 2200 GGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTATCCCTTCCCTGACAGCAGCTGG 2259
QY TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
Db 2260 TATTTTGCACAGAGTCTCATCTTCTACTCTCCCTCAGCCATCTACGGAGCAGTGCC 2319
QY SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2320 AGTTACTCTGCTCAGCTGAGCCAGCTGCCCACTTGGCGAGACCAAGTCTATTCTGTG 2379
QY ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
Db 2380 CGCAGCGCGGAGAACCCAGATGACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGC 2439
QY ProPheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2440 CCCTTTGAAGAGCAGTTTAAACGCAGAGCTGCCAATGGAATTTGGAGAGACATCATG 2499
QY SerGluAsnArgSerArgGluGluGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2500 TCAGAGACAGGTCAAGGAGAGCTGGGAAAGTGGGAGTGGCAGTCACTAGCTTTTCGGGC 2559
QY 510 SerMetGluIleLeuValSer 517
Db 2560 AGCATGGAATCATTTAGGTCTCC 2583
RESULT 9
ABK49402
ID ABK49402 standard; cDNA; 3544 BP.
XX
AC ABK49402;
XX
XX
DT 02-JUL-2002 (first entry)
DE cDNA encoding human dual specificity phosphatase 21117 protein.
XX
KW Human; dual specificity phosphatase 21117; erythroid-related disorder;
KW haematopoietic-related disorder; leukaemia; autoimmune disease; anaemia;
KW erythrocytosis; liver-related disorder; cancer; gene; ss.
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
FT 589..2586
FT /*tag= a
FT /product= "Human dual specificity phosphatase 21117"
FT /note= "Specifically claimed in claim 2"
XX
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PN US2002034807-A1.
XX
PD 21-MAR-2002.
XX
PF 23-MAR-2001; 2001US-00816494.
XX
PR 24-MAR-2000; 2000US-0191858P.
XX
PA (MEYE/) MEYERS R A.
XX
PI Meyers RA;
XX
XX WPI; 2002-351088/38.
DR P-PSDB; ANU79929.
XX
XX New nucleic acids, designated 38692 and 21117, encoding dual specificity
FT phosphatases for treating cell proliferation and differentiation
PT disorders including hematopoietic and erythroid-related disorders and
PT cancers.
XX
XX Claim 2; Fig 1; 76pp; English.
XX
CC The present invention relates to new nucleic acids designated 38692 and
CC 21117 encoding dual specificity phosphatase family members. The nucleic
CC acid, polypeptide encoded by it, and antibody specific for the
CC polypeptide may be used to diagnose and treat haematopoietic-related
CC disorders such as leukaemias and autoimmune diseases, erythroid-related
CC disorders such as anaemias and erythrocytosis, liver-related disorders,
CC and cancers, particularly of the breast, colon, adipose, prostate and
CC lung. The present nucleic acid sequence encodes the human dual
CC specificity phosphatase 21117 protein of the invention, as described
CC above
XX
SQ Sequence 3544 BP; 1000 A; 840 C; 822 G; 892 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 6 Gaps: 0
US-09-964-277-21 (1-517) x ABK49402 (1-3544)
QY 30 GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysProLys 49
Db 1120 GAGCTGATGCAGCAGATGGGATTGGTTATGTTTAAATGCCAGCAATACCTGTCCAAAG 1179
QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 1180 CCTGACTTTATCCCGAGTCTCTCAATTTCTCGTGCCTGTGAATCACAGCTTTTGTGAG 1239
QY 70 LysIleLeuProTyrPheAspLysSerValAspPheIleGlyLysAlaLysAlaSerAsn 89
Db 1240 AAAATTTTGGCGTGGTGGCAATCAGTAGATTTCATTGAGNAAGCAAAAGCTCCAT 1299
QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 1300 GGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGTATCGCC 1359
QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 1360 TACATCATGAGAGAGATGGACATGTCTTTAGATGAAGCTTTACAGATTTGTGAAGAAAAA 1419
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 1420 AGACCTACTATATCTCCAAACTTCAATTTTCTGGCCAACTCTCGGACTATGAGAGAG 1479
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu 169
Db 1480 ATTAAGAACCAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTGTCTGCACCTGGAG 1539
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Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
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Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1660 GCCAGCGTGCACCGCTGCCAGCGTGCAGCGCTGCTGTTAGAGGACAGCCCGCTGGTA 1719
Qy 230 GlnAlaLeuSerClyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1720 CAGCGCTCAGTGGGCTGCACTCTGCCGAGACAGCTGGGAAGACAGCAATAAGCTCAAG 1779
Qy 250 ArgSerPheSerLeuAspLysSerValSerAlaSerMetAlaAlaSerLeu 269
Db 1780 CGTTCCTCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTA 1839
Qy 270 HisGlyPheSerSerSerGluAspAlaLeuGlyTyrLysProSerThrThrLeuAsp 289
Db 1840 CATGGCTTCTCCTCATCAGAAATGCTTGGAAATACTACAAACCTTCCACTACTCTGGAT 1899
Qy 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1900 GGGACCAACAAGCTATGCCAGTCTCCCTGTTCAAGGAACATATCGAGCAGACTCCGAA 1959
Qy 310 ThrSerProAspLysGluGluAlaSerLeuProLysLysLeuGlnThrAlaArgProSer 329
Db 1960 ACCAGTCCCTGATAAGAGGAGAACGACATCCCAAGAGCTGCAGACCGCAGCGCTTCA 2019
Qy 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
Db 2020 GACAGCAGACAGCAAGCATTGATTCGGTCAGAACAGCAGCAGCTGGCACCCCGCAGGG 2079
Qy 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 2080 TCCCTTTTATCTCCACTGCATCGAAGTGGAGCGGTGGAGGACAAATTACACACAGCTTC 2139
Qy 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 2140 CTTTTCGGCTTTCCACGACGACGACGACCTACGAAAGTCTGCTGGCTGGCTTAAAG 2199
Qy 390 GlyTrpHisSerAspLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
Db 2200 GGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACACAGAGCTGG 2259
Qy 410 TyrPheAlaThrGluSerSerHisPheThrSerAlaSerAlaIleTyrGlySerAla 429
Db 2260 TATTTTGCACAGAGTCCACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTGCC 2319
Qy 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2320 AGTTACTCTGCTACAGCTGCAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTG 2379
Qy 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
Db 2380 CGCAGGCGGAGAGGCAAGTGCAGAGCTGACTCGCGCGAGCTGGCATGAAGAGAGC 2439
Qy 470 ProPheGlyLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2440 CCTTTGAAGAGAGGTTTAAACGAGAACTGCCAAATGGAAATTTGGAGAGCATCATG 2499
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2500 TCAGAGAACAGGTACGCGGAAGAGCTGGGGAAAGTGGGCAGTCACTAGCTTTTCGGGC 2559
Qy 510 SerMetGluIleLeuGluValSer 517
Db 2560 AGCATGAAATCATTAGGTCTCC 2583
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RESULT 10

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ABK14474
ID ABK14474 standard; cDNA; 3766 BP.
XX
AC ABK14474;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human protein phosphatase 7 (PP7) cDNA sequence.
XX
KW Human; protein phosphatase 7; PP7; immune system disorder; AIDS;
KW acquired immunodeficiency syndrome; thymic hypoplasia; anaemia; asthma;
KW Crohn's disease; neurological disorder; epilepsy; Huntington's disease;
KW dementia; Parkinson's disease; developmental disorder; Down's syndrome;
KW cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma;
KW melanoma; myeloma sarcoma; gene; ss.
XX
OS Homo sapiens.
XX
FH Key' Location/Qualifiers
CDS 538..2535
FT /*tag= a
FT /product= "protein_phosphatase_7_(PP7)"
XX
NC_0200210363-A2.
XX
PD 07-FEB-2002.
XX
PF 26-JUL-2001; 2001WO-US023716.
XX
PR 28-JUL-2000; 2000US-0221679P.
PR 03-AUG-2000; 2000US-0223272P.
PR 10-AUG-2000; 2000US-0224309P.
PR 18-AUG-2000; 2000US-0226728P.
PR 30-AUG-2000; 2000US-0229254P.
PR 08-SEP-2000; 2000US-0231366P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Tang YT, Elliott VS, Ramkumar J, Yao MG, Burford N, Wang YE;
PI Stewart EA, Gandhi AR, Patterson C, Lee EA, Hafalia AJA, Lu DAM;
PI Tribouley CM, Griffin JA, Baughn MR, Yue H, Warren BA, Nguyen DB;
PI Walla NK, Kearney L;
XX
XX WPI; 2002-188735/24.
DR P-PSDB; AAU75789.
XX
XX New protein phosphatases, useful for diagnosing, treating or preventing
XX immune system disorders (e.g. Crohn's disease), neurological disorders
XX (e.g. Parkinson's disease), or cell proliferative disorders (e.g.
XX cancers).
XX
XX Claim 5; Page 114-115; 117pp; English.
XX
XX The present invention relates to a new polypeptide, a naturally occurring
XX amino acid sequence at least 95 % identical to it, a biologically active
XX fragment of it or an immunogenic fragment of it. The polypeptides,
XX polynucleotides, agonists and antagonists are useful for diagnosing,
XX treating or preventing disorders associated with aberrant expression of
XX protein phosphatases (PP), particularly immune system disorders e.g.
XX acquired immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia,
XX asthma or Crohn's disease, neurological disorders e.g. epilepsy,
XX Huntington's disease, dementia or Parkinson's disease, developmental
XX disorders e.g. Down's syndrome, or cell proliferative disorders e.g.
XX cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma
XX or sarcoma. The present nucleic acid sequence encodes human protein
XX phosphatase 7 (PP7) which is one of several human protein phosphatases
XX (AAU75783-AAU75792) of the invention
XX
XX Sequence 3766 BP; 1011 A; 903 C; 918 G; 934 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 0 Length: 3766
Score: 488.00 Matches: 488

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.39%	Indels:	0
DB:	6	Gaps:	0
US-09-964-277-21 (1-517) x ABK14474 (1-3766)			
QY	30	GluLeuMetGlnGlnAsnGlyLeuGlyTyrValLeuAsnAlaSerAsnThrCysProLys	49
DB	1069	GAGCTGATGCGAGCAAAATGGGATGGTTATGTTAAATCCAGCAATACCTGTCCAAAG	1128
QY	50	ProAspPheLeuProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu	69
DB	1129	CCTGACTTTATCCCGAGTCTCAITTCCTGCGTGTGCTGTGATGACACTTTTGTGAG	1188
QY	70	LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn	89
DB	1189	AAAATTTTTCGCGTGTTCGACAAATCATGATGATTTCAITTGAGAAGCAAAAGCTCCCAAT	1248
QY	90	GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla	109
DB	1249	GGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC	1308
QY	110	TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys	129
DB	1309	TACATCATGAAGAGATGGACATGTCTTTAGATCAAGCTTACAGATTGTGAAAAGAAAA	1368
QY	130	ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys	149
DB	1369	AGACTTACTATCTCCAAATCTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAGAAG	1429
QY	150	IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu	169
DB	1429	ATTTAGAACCAAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTCTGACCTGGAG	1488
QY	170	LysProAsnGluProValProAlaValSerGluClyGlyGlnLysSerGluThrProLeu	189
DB	1489	AAGCCAAATGAACCTGTCTCCCTGCTGTCTCAGAGGGTGGACAGAAAACGAGACGCCCTC	1548
QY	190	SerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro	209
DB	1549	AGTCACCCCTGTGCGACTCTGCTACTCAGAGCGCAGCAGCAAGGCCCGTGCATCCC	1608
QY	210	AlaSerValProSerValProSerValGlnProSerLeuLeuAspSerProLeuVal	229
DB	1609	GCCAGCGTCCCGAGCGTCCCGAGCGTGCAGCGTCTGCTGTAGAGGACAGCCCGCTGTA	1668
QY	230	GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys	249
DB	1659	CAGGCGCTCAGTGGCTGCACCTGTCCGACAGAGGCTGGAAGACAGCAATAGCTCAAG	1728
QY	250	ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu	269
DB	1729	CGTTCCTTCTCTGATATCAATCAATCAGTTTCAATTCAGCCAGCATGGCAGCATCTTA	1788
QY	270	HisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp	289
DB	1789	CATGCTCTTCTCATCAGAGATGCTTTTGAATACTACAAACCTTCCACTCTCGGAT	1848
QY	290	GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu	309
DB	1849	GGGACCAACAGCTATGCCAGTTCTCCCTGTTCCAGGACTATCCGAGCAGATCCCGAA	1908
QY	310	ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer	329
DB	1909	ACCAGTCTGTATAGAGAGAGCAGCATCCCAAGAGAGCTGCAGACCGCCAGCCCTTCA	1968
QY	330	AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg	349
DB	1969	GACAGCCAGACGAGATTCATTCGTTCCGTCAGAACAGAGAGTGGCCACCGCCCGAGG	2028
QY	350	SerLeuLeuSerProLeuHisArgSerGlySerValGluAspSerTyrHisThrSerPhe	369
DB			

Db	2029	TCCCTTTTATCTCCACTGTCATCGAAGTGGGAGCGTGGAGACAATTACACACAGCTTC	2088
QY	370	LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys	389
DB	2089	CTTTTCGGCTTTCCACCCAGCAGCAGCAGCTCAGAAAGTCTGCTGGCCTGGCCCTTAAG	2148
QY	390	GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp	409
DB	2149	GGCTGGCAGCTCGGATATCTTTGGGCCCCCAGACCTCTACCCCTTCCCTGACCCAGCTGG	2208
QY	410	TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla	429
DB	2209	TATTTTGCACAGAGTCTCTCACTTCTACTCTGCTCAGCCATCTACGGAGCAGCTGCC	2268
QY	430	SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal	449
DB	2269	AGTTACTCTGCTACAGCTGCAGCCAGCTCCCACTTGGGAGACCAAGTCTATTCTGTG	2328
QY	450	ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer	469
DB	2329	CGCAGCGCGCAGAGCAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGGC	2388
QY	470	ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMet	489
DB	2389	CCCTTTGAAAAGCAGTTTAAACCGCAGAAAGCTGCCAAATTCGAATTTGGAGAGCATATG	2448
QY	490	SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly	509
DB	2449	TCAGAGAACAGGTCACGGGAGAGCTGGGGAAGTGGGCAAGTGCAGTCTAGCTTTTCGGGC	2508
QY	510	SerMetGluIleIleGluValSer	517
DB	2509	AGCATGGAAATCATTTAGGTCTCC	2532
RESULT 11			
ABN83966 standard; DNA; 4790 BP.			
ID	ABN83966		
XX	AC	ABN83966;	
DT	06-SEP-2002	(first entry)	
XX	XX	Human gene sequence #13.	
DE	Human	gene	
XX	Human	brain; tonsil; hippocampus; foetal brain; diagnosis; gene; ds.	
KW	Human	sapiens.	
OS	Homo	sapiens.	
XX	Key	Location/Qualifiers	
PH	CDS	184..2181	
FT		/*tag= a	
XX	WO200252005-A1.		
PN	04-JUL-2002.		
XX	20-DEC-2001;	2001WO-JP011217.	
XX	22-DEC-2000;	2000JP-00389742.	
XX	(KAZU-)	KAZUSA DNA RES INST FOUND.	
PA	(CELE-)	CELESTAR LEXICO-SCI LTD.	
XX	Ohara O,	Nagase T, Nakajima D;	
PI	WPI;	2002-500762/53.	
XX	P-PSDB;	ABB97946.	
DR	Genes and their expression products cloned from human cDNA libraries for		
XX	treatment and diagnosis of diseases associated with their expression.		
PS	Claim 1(a); Page 111-117; 238pp; Japanese.		
XX			

CC The invention relates to DNA encoding polypeptides directly cloned from
 CC cDNA libraries originating in adult whole brain, human tonsil, human
 CC adult hippocampus and human foetal whole brain. Polypeptides and
 CC polynucleotides of the invention may be used in the investigations of
 CC differential expression of the DNA sequences in normal subjects and
 CC disease patients. They may also be used in the production of antibodies,
 CC oligonucleotide probes and DNA chips for diagnosis and identification of
 CC drugs for treatment of diseases with which the DNA sequences are
 CC associated. The sequences given in records ABN83954-ABN83984 represent
 CC human gene sequences of the invention
 XX

SQ Sequence 4790 BP; 1293 A; 1064 C; 1152 G; 1281 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 4790
 Score: 488.00 Matches: 488
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.39% Indels: 0
 DB: 6 Gaps: 0

US-09-964-277-21 (1-517) x ABN83966 (1-4790)

QY 30 GluLeuMetGlnGlnAsnGlyLeuGlyTyrValLeuAsnAlaSerAsnThrCysProlys 49
 DB 715 GAGCTGATGAGCAGAAATGGATTGTTATGTTAAATGCCAGCAATACCTGTCCAAAG 774
 QY 50 ProAspPheLeuProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
 DB 775 CCTGACTTATCCCGAGTCTCATTTCCCGTGTCCTGTGAAATGACAGCTTTGTGAG 834
 QY 70 LysileLeuProThrLeuAspLysSerValAspPheLeuGlyLeuAlaLysAlaSerAsn 89
 DB 835 AAAATTTTGGCGTGTGGCAAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCTCCCAAT 894
 QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
 DB 895 GGAATGTTCTAGTGCACTGTTTAGTGGGATCTCCCGCTCCGCCACCATGCTATCGCC 954
 QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
 DB 955 TACATCATGAGAGGATGGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAA 1014
 QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
 DB 1015 AGACCTACTATATCTCCAACTTTCAATTTCTGGGCCAACTCTGAGCTATGAGAAGAAG 1074
 QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
 DB 1075 ATTAAGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAGCTGCTGCTGGAG 1134
 QY 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
 DB 1135 AAGCCAAATGAACCTGTCTCCCTGTCTGCTCAGAGGGTGGACAGAAAAAGCAGAGCCCTC 1194
 QY 190 SerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
 DB 1195 AGTCCACCTGTGCGGACTCTGCTACTCTAGAGCAGAGGACAAAGGCCCTGTGATCCC 1254
 QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
 DB 1255 GCCAGGTGCCAGCGTGGCCAGCGTGGTGTGCTGCTGAGGAGGACAGCCGCTGGTA 1314
 QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLysLys 249
 DB 1315 CAGCGCTCAGTGGGCTGCACTGTCCGGCAGACAGGCTGGAAGACAGCAATTAAGCTCAAG 1374
 QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
 DB 1375 CGTTCCTTCTCTGGATATCAATCAGTTTCATATTCAGCCAGCATGCGAGCATCCITA 1434
 QY 270 HisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289

DB 1435 CATGGCTTCTCTCATCAGAAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTCGAT 1494
 QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGlnLeuSerGluGlnThrProGlu 309
 DB 1495 GGGACCAACAAGCTATGCCAGTTCTCCCTGTTTCCAGGAAGCTATCGGAGCAGATCCGAA 1554
 QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
 DB 1555 ACATGCTCTGATAGGAGAGAGCAGCATCCCCAAGAAGCTGCAGACCGCAGGCTTCA 1614
 QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
 DB 1615 GACGCCAGCAGCAGCGATTGCTTCGTTCAGAACCCAGCAGCAGTGGCAGCGCCAGAGG 1674
 QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
 DB 1675 TCCCTTTTATCTCCACTCATCGAAGGGGAGCGTGGAGACAATTACCAACAGCTTC 1734
 QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
 DB 1735 CTTTTCGGCTTTCCACCAGCAGCAGCACCTCAGAAAGTCTGCTGGCCTGGGCTTTAAG 1794
 QY 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTip 409
 DB 1795 GGTGGCTGCTCGGATATCTTGCCCCCGAGACCTTACCCCTTCCCTGACCAGCAGCTGG 1854
 QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
 DB 1855 TATTTTGGCAGAGTCTCTCACATTTCTACTCTGCTCAGCCATCTACGGAGGAGTGCC 1914
 QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
 DB 1915 AGTACTCTGCTGACGTGCGAGCAGCTGCCACTTGGCGAGACCAAGTCTATCTGTG 1974
 QY 450 ArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
 DB 1975 CGCAGCGCGCAGAACCAAGTACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGAGC 2034
 QY 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
 DB 2035 CCCTTTGAAAGCAGTTTAAACGCCAAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATG 2094
 QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
 DB 2095 TCAGAACAGCTTCAGGGAAGAGCTGGGAAAGTGGGCAAGTCACTAGCTTTTCGGGC 2154
 QY 510 SerMetGluIleIleGluValSer 517
 DB 2155 AGCATGGAATCATTGAGGTCTCC 2178

RESULT 12

ABV20833
 ID ABV20833 standard; cDNA; 5145 BP.

XX AC ABV20833;
 XX 13-SEP-2002 (first entry)

DT XX Human prostate expression marker cDNA 20824.

DE XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.
 XX FN WO200160860-A2.

XX XX 23-AUG-2001.

XX XX 20-FEB-2001; 2001WO-US005171.

XX XX 17-FEB-2000; 2000US-0183319P.

XX XX 16-MAR-2000; 2000US-0189662P.

AC ABV21080;
XX
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 21071.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
XX W02001:60860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
XX
XX 25-MAY-2000; 2000US-0207454P.
XX
XX 09-JUN-2000; 2000US-0211314P.
XX
XX 18-JUL-2000; 2000US-0219007P.
XX
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 3481; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 5 Gaps: 0

US-09-964-277-21 (1-517) x ABV21080 (1-5145)

QY 30 GluLeuMetGlnGlnAsnGlyLeuGlyTyrValLeuAsnAlaSerAsnThrCysProlys 49
Db 1120 GAGCTGATGCAGCAGAAATGGATGGTTATGTTAAATGCCAGCAATACCTGTCCTCAAG 1179
QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 1180 CCTGACTTTATCCCGAGTCTCATTTCCCGGTGGCTGTGAATGACAGCTTTTGTGAG 1239
QY 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLeuAlaLysAlaSerAsn 89
Db 1240 AANAATTGCGGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAGCCCTCCAAAT 1299

QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 1300 GGAATGTTCTAGTGCATCTGTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC 1359
QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 1360 TACATCATGAAGAGATGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAGAAAAA 1419
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 1420 AGACCTACTATATCTCCAACTTCATTTTCTGGCCDACTCTCTGGACTATGAGAAGAG 1479
QY 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisGluGlu 169
Db 1480 ATTAAGAACACGACTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTGCTGCACCTGGAG 1539
QY 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
Db 1540 AAGCCAAATGAACCTGTCTCTGCTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTC 1599
QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
Db 1600 AGTCCACCTGTGCGGACTCTGTACTCTCAGAGCGAGGAGCAAAAGGCCCGTGCATCCC 1659
QY 210 AlaSerValProSerValProSerValGlnProSerIleLeuGluAspSerProLeuVal 229
Db 1660 GCCAGCGTCCCGAGCGTCCCGAGCTGCTGCTGTTAGAGGACAGCCCTCGTA 1719
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1720 CAGGCGCTCAGTGGCTGCACCTGTCCGACAGAGCTGGAGAGACAGCAATAAGCTCAAG 1779
QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
Db 1780 CGTTCCTCTCTCTGGATATCAAAATCAGTTTCATATTACAGCCAGCATGGCAGCATCCTTA 1839
QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1840 CATGGCTTCTCTCTATCAGAGATGCTTTGGAATACTACAAACCTTCACACTCTCGAT 1899
QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1900 GGGACCAACAAGCTATGCGAGTTCTCCCTCTTCAGGAACCTATCGAGAGACACTCCCGAA 1959
QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1960 ACCAGTCTGATAAGAGAGAGAGCCAGCAGCTCCCAAGAGCTGCAGACCCCGAGCCCTTCA 2019
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
Db 2020 GACGCCAGAGCAAGGATTGCAITTCGTCAGAACCCAGCAGCAGTGGCAGCCCGCAGAGG 2079
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 2080 TCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGCAATATCCACACAGCTTC 2139
QY 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLysLys 389
Db 2140 CTTTTGCGCTTTCCACCAGCAGCAGCACTCAGAAAGTCTGCTGGCTGGGCTTAAG 2199
QY 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
Db 2200 GGTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCTGACCCAGAGCTGG 2259
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysAla 429
Db 2260 TATTTGGCACAGAGTCTCTACATTTCTGCTTCAGCCATCTACGAGGAGGAGTGGC 2319
QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2320 AGTTACTCTGCTACAGCTGCAGCGAGCTGCCACTTGGCGAGAGCAAGTCTATTCTGTG 2379
QY 450 ArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469

Db 2380 CCACGGGGCAGACCCAGTGCACAGCTGACTCGCGCGGAGCTGGCATGAAGAGC 2439
QY 470 PropheGluLysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2440 CCCTTTGAAACGAGCTTTAAACGCAGAGCTGCCAAATGGAATTTGGAGAGCATCATG 2499
QY 490 SerGluAenArgSerArgGluLuleuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2500 TCAGAGACAGTCTACGGGAGAGCTGGGAAATGGGCAGTCACTAGCTATTTTCGGGC 2559
QY 510 SerMetGluIleleGluValSer 517
Db 2560 AGCATGGAATCATTTAGGTCTCC 2583
RESULT 14
ABV26680
ID ABV26680 standard; cDNA; 5145 BP.
XX
AC ABV26680;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 26671.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0198862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5388-5389; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
CC specification or its complement. (II) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 488.00 Matches: 488

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 5 Gaps: 0
US-09-964-277-21 (1-517) x ABV26680 (1-5145)
QY 30 GluLeuMetGlnGlnAenGlyIleGlyTyrValLeuAenAlaSerAenThrCysProLys 49
Db 1120 GAGCTGATGCACGAGAATGGGATTTGTTATGTGTTAAATCCACGCAATACCTGTCCAAAG 1179
QY 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 1180 CCGTACTTATCCCGAGTCTCATTTCTCGGTGCTGTGAATGACAGCTTTTGTGAG 1239
QY 70 LysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAen 89
Db 1240 AAAATTTTGGCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAGCGCTCCAAT 1299
QY 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 1300 GGATGTGTTCTAGTGCACCTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGGTATCGCC 1359
QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 1360 TACATCATGAAGAGATGGACATGCTCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAA 1419
QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 1420 AGACTACTATATCTCCAAACTTCAATTTCTCGGCCAACTCCTCGACATATGAGAAGAAG 1479
QY 150 IleLysAenGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
Db 1480 ATTAAGAACCAGACTGGAGCATCAGGGCCAAAGGCAAACTCAAGCTGTCACCTGGAG 1539
QY 170 LysProAenGluProValProAlaValSerGlyGlyGlnLysSerGluThrProLeu 189
Db 1540 AAGCCAAATGAACCTGTCCTGTCTCAGAGGGTGGAGAGAAAGCGAGAGCGCCCTC 1599
QY 190 SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro 209
Db 1600 AGTCACCTGTGCGGACTCTGCTACTCAGAGCGAGCAGGCAAGAGCCGCTGCATCCC 1659
QY 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1660 GCCAGCGTGCACGCGTGCAGCGCTGCTGTTAGAGCAGCAGCGCGCTGGTA 1719
QY 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLysLys 249
Db 1720 CAGCGCTCAGTGGCTGCACCTGTCGCGAGAGCTGGAAGACAGCAATAGCTCAAG 1779
QY 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
Db 1780 CGTTCCCTTCTCTGGGATATCAAAATCAGTTTCATATTACGCCAGCATGGCAGCATCTTA 1839
QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1840 CATGGCTTCTCCTCATCAGAAGATGCTTTGGAAATACTACAAACCTTTCCTACTCTGGAT 1899
QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGlnLeuSerGluGlnThrProGlu 309
Db 1900 GGGACCAACAGCTATGCCAGTCTCCCTGTCAGGAATATCGAGCAGACTCCCGAA 1959
QY 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1960 ACCAGTCTCTATGAAGGAGGAGCAGCATCCCCAGAGCTGCAGACCCGCGGCTTCA 2019
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArg 349
Db 2020 GACAGCGAGCAAGGATTTGCATTCTGGTCAAGACCGAGCAGAGTGGCACCGCCAGAGG 2079
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369

2080	TCCTCTTTATCTCCACTGCAATCGAAGTGGAGCGTGGAGGACAATACACACAGCTTC	2139
370	LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLySerAlaGlyLeuGlyLeuLys	389
2140	CTTTTCGGCCCTTCCACGAGCAGCAGCAGCTCAGCAAGTCTGCTGGCTGGGCTTAAAG	2199
390	GlyTTPHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTTP	409
2200	GGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCTGACGAGCAGCTGG	2259
410	TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla	429
2260	TATTTTGGCCACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGGAGCAGTGCC	2319
430	SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal	449
2320	AGTTACTCTGCTCTACAGCTGAGCAGCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTG	2379
450	ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTTPHisGluGluSer	469
2380	CCGAGCGGCGAGAGCCAGTGCACAGAGCTGACTCGCGCGGAGCTGGCATGAGAGAGC	2439
470	ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet	489
2440	CCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGCAATTTGGAGAGCATCATG	2499
490	SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly	509
2500	TACAGAGACAGGTACGGGAAAGAGCTGGGAAAAGTGGGAGTCAGTCTAGCTTTTCGGGC	2559
510	SerMetGluIleIleGluValSer	517
2560	AGCATGGAAATCATTTAGGCTCTCC	2583
RESULT 15		
ABV20978		
ID	ABV20978 standard; cDNA; 5145 BP.	
XX	AC	ABV20978;
XX		
DT	13-SEP-2002 (first entry)	
XX		
DE	Human prostate expression marker cDNA 20969.	
XX		
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynanamic marker;	
KW	pharmacogenomic marker; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200160860-A2.	
XX		
PD	23-AUG-2001.	
XX		
PF	20-FEB-2001; 2001WO-US005171.	
XX		
PR	17-FEB-2000; 2000US-0183319P.	
PR	16-MAR-2000; 2000US-0189862P.	
PR	25-MAY-2000; 2000US-0207454P.	
PR	09-JUN-2000; 2000US-0211314P.	
PR	18-JUL-2000; 2000US-0219007P.	
PR	13-DEC-2000; 2000US-0255281P.	
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX		
PI	Schlegel R, Endege WO, Monahan JE;	
XX		
DR	WPI; 2001-662795/76.	
XX		
PT	Novel isolated nucleic acid molecule associated with cancerous state of	
PT	prostate cells and correlating with presence of prostate cancer, useful	
PT	for detecting presence of prostate cancer, stage of prostate cancer.	
XX		
PS	Claim 1; Page 3451; 11750pp; English.	

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or incidence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 5 Gaps: 0

US-09-964-277-21 (1-517) x ABV20978 (1-5145)

QY	30	GlulLeuMetGlnGlnAnGlylleGlyTyrValLeuAsnAlaSerAsnThrCysProLys	49
DB	1120	GAGCTGATGCAGCAGAAATGGATGGTTATGTGTTAATGCCAGCAATACCTGTCTCCAAAG	1179
QY	50	ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu	69
DB	1180	CGTGACTTATCCCGGAGTCTCAATTCCTCGCTGCTGTGAATGACAGCTTTTGTGAG	1239
QY	70	LysIleLeuProTyrLeuAspLysSerValAspPheIleGluValAlaValAlaSerAsn	89
DB	1240	AAATTTTCGCGTGGTGGCAAAATCAGTAGATTTCTTGGAAAGCAAAAGCCTCCCAT	1299
QY	90	GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla	109
DB	1300	GGATGTGTTCAGTGCACTGTTTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC	1359
QY	110	TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys	129
DB	1360	TACATCATGAAGAGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAA	1419
QY	130	ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys	149
DB	1420	AGACCTACTATATCTCCAACTTCATTTCTGGGCCAACTCTCTGGACTATGAGAAGAAG	1479
QY	150	IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu	169
DB	1480	ATTAAGAACCAAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTCACCTGGAG	1539
QY	170	LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu	189
DB	1540	AAGCCAAATGAACCTGTCCCTGCTCTCAGAGGGTGGACAGAAAGCGACGACGCCCTC	1599
QY	190	SerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisPro	209
DB	1600	AGTCCACCTGTGCGGACTCTGCTACCTCAGAGCGAGCAGGACAAAGGCCCGCTGCATCCC	1659
QY	210	AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal	229
DB	1660	GCACGCTGCCACGCTGCCACGCTGACCGCTCGCTGTTAGAGACAGCCCGCTGGTA	1719
QY	230	GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys	249
DB	1720	CAGCGCTCAGTGGCGCTGCACCTGTCGCGACAGCAGGCTGGAGACAGCAATTAAGCTCAAG	1779
QY	250	ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu	269
DB	1780	CGTCTCTCTCTCGATATCAATCAGTTTCATATTATTCAGCAGCATGCGACATCTCTTA	1839

QY 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1840 CATGGCTTCTCTCATCAGAGATCTTTGGAAATACTACAAACCTTCCACTACTCTGGAT 1899
QY 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1900 GGGACCAACAAGCTATGCCAGTTCTCCCTGTTTCAGGAACCTATCGGAGCAGACTCCCGAA 1959
QY 310 ThrSerProAspLysGluGluAlaSerLeProLysLysLeuGlnThrAlaArgProSer 329
Db 1960 ACCAGTCTCTGATAGAGAGAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCA 2019
QY 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerSerGlyThrAlaGlnArg 349
Db 2020 GACAGCCAGAGCAAGCATTTGCATTGGTTCAGACCCAGCAGTGGACCGCCAGAGG 2079
QY 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 2080 TCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGACAATTACCAACCCAGCTTC 2139
QY 370 LeuPheGlyLeuSerThrSerClnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLys 389
Db 2140 CTTTTCGGCCCTTCCACAGCCAGCAGCACCCTCACGAAGTCTGCTGGCCTGGGCCCTTAAG 2199
QY 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
Db 2200 GGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGG 2259
QY 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlySerAla 429
Db 2260 TATTTTGCCACAGAGTCTCCACCTTCTACTCTCCCTCAGCCATCTACGGAGGAGCTGCC 2319
QY 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2320 AGTTACTCTGCTCAGCTGAGCCAGCTGCCACTTGGGAGACCAGTCTATTCTGTG 2379
QY 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
Db 2380 CGCAGCGGCGAGAAGCCCAAGTGCAGAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGC 2439
QY 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2440 CCCTTTGAAGAAGCAGTTTAAACGGCAGAGCTGCCAAATGGAAATTGGAGAGAGCATCATG 2499
QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2500 TCAGAGAACAGGTCAAGGGAAGAGCTGGGAAAGTGGGAGTCAAGTCTAGCTTTTCGGGC 2559
QY 510 SerMetGluIleIleGluValSer 517
Db 2560 AGCATGGAAATCATGTAGGCTCTCC 2583

Search completed: February 28, 2004, 01:26:16
Job time : 621 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2004, 18:43:58 ; Search time 222 seconds
(without alignments)
8329.263 Million cell updates/sec

Title: US-09-964-277-20

Perfect score: 3332

Sequence: 1 gagagaaggagaagataata.....ataaagatgaactgtgttc 3332

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2950	88.5	3544	US-09-816-494-1	Sequence 1, Appli
2	1660	49.8	1998	US-09-816-494-3	Sequence 3, Appli
3	247	7.4	279	US-09-016-434-91	Sequence 91, Appli
4	225.2	6.8	2377	US-09-920-668-3	Sequence 1, Appli
5	109.6	3.3	1830	US-09-557-921-1	Sequence 3, Appli
6	95	2.9	2303	US-09-922-146-3	Sequence 347, App
7	94.6	2.8	1208	US-09-023-655-347	Sequence 1135, App
8	90.2	2.7	2109	US-09-016-434-1135	Sequence 946, App
9	90.2	2.7	2109	US-09-023-655-946	Sequence 776, App
10	86.2	2.6	240	US-09-016-434-776	Sequence 801, App
11	85.6	2.6	1619	US-09-702-705-801	Sequence 801, App
12	85.6	2.6	1619	US-09-736-457-801	Sequence 801, App
13	85.6	2.6	1619	US-09-614-124B-801	Sequence 801, App
14	85.6	2.6	1619	US-09-671-325-801	Sequence 801, App
15	85.6	2.6	1619	US-09-589-184-801	Sequence 804, App
16	85.6	2.6	4637	US-09-702-705-804	Sequence 804, App
17	85.6	2.6	4637	US-09-736-457-804	Sequence 804, App
18	85.6	2.6	4637	US-09-614-124B-804	Sequence 804, App
19	85.6	2.6	4637	US-09-671-325-804	Sequence 804, App
20	85.6	2.6	4637	US-09-589-184-804	Sequence 804, App
21	84	2.5	1238	US-08-530-290-11	Sequence 11, Appli
22	84	2.5	1238	US-09-702-705-803	Sequence 803, App
23	84	2.5	1238	US-09-736-457-803	Sequence 803, App
24	84	2.5	1238	US-09-614-124B-803	Sequence 803, App
25	84	2.5	1238	US-09-671-325-803	Sequence 803, App
26	84	2.5	1238	US-09-589-184-803	Sequence 803, App
27	84	2.5	2064	US-09-702-705-825	Sequence 825, App

28	84	2.5	2064	US-09-736-457-825	Sequence 825, App
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35	84	2.5	2109	US-09-671-325-826	Sequence 826, App
36	84	2.5	2109	US-09-589-184-826	Sequence 826, App
37	84	2.5	2240	US-09-016-434-1100	Sequence 1100, Ap
38	82	2.5	2000	US-09-016-434-1291	Sequence 1291, Ap
39	81.2	2.4	1987	US-08-990-379-1	Sequence 1, Appli
40	81.2	2.4	1993	US-08-990-379-2	Sequence 2, Appli
41	80.4	2.4	944	US-09-371-671B-10	Sequence 10, Appli
42	71.6	2.1	539	US-09-389-681-311	Sequence 311, App
43	71.6	2.1	539	US-09-620-405B-311	Sequence 311, App
44	71.6	2.1	539	US-09-339-338-311	Sequence 311, App
45	71.6	2.1	539	US-09-433-826B-311	Sequence 311, App

ALIGNMENTS

RESULT 1
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)....(2583)
US-09-816-494-1

Query Match	88.5%	Score 2950;	DB 4;	Length 3544;
Best Local Similarity	95.0%	Pred. No. 0;		
Mismatches	3135;	Conservative	0;	Mismatches 165; Gaps 2;
QY	197	CGTTTCAGTCAGTGTAAAGCTGTTGGAGCGCGGAGCAAGTAAGTAAGTGAATG	256	
DB	224	CGTTTCAGTCAGTGTAAAGCTGTTGGAGCGCGGAGCAAGTAAGTAAGTGAATG	283	
QY	257	CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAAATGGTATTCCAGTCATCTCTTTATGA	316	
DB	284	CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAAATGGTATTCCAGTCATCTCTTTATGA	343	
QY	317	ATCAAAATGTAGGGGCTGCTTTGTGGAGCGAGTCCCTTTGCAAGACACATCAACGGGAAA	376	
DB	344	ATCAAAATGTAGGGGCTGCTTTGTGGAGCGAGTCCCTTTGCAAGACACATCAACGGGAAA	403	
QY	377	GAGAAAGACATTCACCTTGAGGGCTCTTGTGAAATGGGTTTAACTCTCTTTTGGC	436	
DB	404	GAGAAAGACATTCACCTTGAGGGCTCTTGTGAAATGGGTTTAACTCTCTTTTGGC	463	
QY	437	AGTCACCACCAAGCTGACCTCATACATTTTAGTACAAATGAGTGGCTGAGCCTTTGAGC	496	
DB	464	AGTCACCACCAAGCTGACCTCATACATTTTAGTACAAATGAGTGGCTGAGCCTTTGAGC	523	
QY	497	ACACCAACCATACATCTCGTGCACAAATTAAGAGAGGTGGGAAAGAGGACTTATTG	556	

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Qy 557 TTGTCATGCCCCATGATGATGGAACCAAAATGTTACTGAGAGGTGGTGGCTGCG 616
Db 584 TTGTCATGCCCCATGATGATGGAACCAAAATGTTACTGAGAGGTGGTGGCTGCG 643
Qy 617 TGAAGATGGAACGGAAGGAGTCTGCTAAATGATAGCCGGCCATTGTTGGAATACAAATA 676
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Qy 927 ----- 926
Db 1004 AATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTTGGC 1063
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Qy 1173 TCATGAAGAGGATGGACATGCTTTTAGATGAAGCTTTACAGATTTGTGAAGAAAGAAAGAC 1232
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Qy 1413 CACCTGTGCGGACTGCTGCTACCTCAGAGGCGAGCAAAAGCGGCTGCTGCTCCGCCA 1472
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Qy 1593 CTTCTCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTCTTACATG 1652
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Qy 1773 GTCTGTATAAGGAGGAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTTCAGACA 1832
Db 1964 GTCTGTATAAGGAGGAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTTCAGACA 2023
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Db 2024 GCCAGAGCAAGCGATTGCAATTCGGTTCAGAACCTATTCGGAGCAGACTCCCGAGAGTCCC 2083
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Db 2084 TTTTATCTCCACTGATCGAAGTGGAGCGTGGAGGCAATTTACACACAGCTTCCTTT 2143
Qy 1953 TGGGCTTTTCCACCAGCAGCAGCACTTCAGCAAGTCTGCTGGCTCGGCTTAAAGGCT 2012
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Qy 2013 GGCACCTGGATATCTTGGCCCCCAGACTCTACCTTCCCTGACCCAGCAGCTGCTAT 2072
Db 2204 GGCACCTGGATATCTTGGCCCCCAGACTCTACCTTCCCTGACCCAGCAGCTGCTAT 2263
Qy 2073 TTTGCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTCCAGT 2132
Db 2264 TTTGCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTCCAGT 2323
Qy 2133 ACTTGCCTTACAGCTGCAGCCAGCTGCCCATCTTGGGAGACCAAGTCTATTTCTGTGGCA 2192
Db 2324 ACTTGCCTTACAGCTGCAGCCAGCTGCCCATCTTGGGAGACCAAGTCTATTTCTGTGGCA 2383
Qy 2193 GCGCGCAGAAAGCCAAAGTGACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGCCCT 2252
Db 2384 GCGCGCAGAAAGCCAAAGTGACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGCCCT 2443
Qy 2253 TTTGAAAGCAGTTTAAACGCGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2312
Db 2444 TTTGAAAGCAGTTTAAACGCGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCAG 2503
Qy 2313 AGACAGAGTTCAGCGAGAGCTGGGGAAGTGGGAGTCACTGCTAGCTTTTCGGGCGAGCA 2372
Db 2504 AGACAGAGTTCAGCGAGAGCTGGGGAAGTGGGAGTCACTGCTAGCTTTTCGGGCGAGCA 2563
Qy 2373 TGGAAATCAATTGAGTCTCTCTGAGAAAGAAAGACACTTGTGACTTCTATAGACAAATTTT 2432
Db 2564 TGGAAATCAATTGAGTCTCTCTGAGAAAGAAAGACACTTGTGACTTCTATAGACAAATTTT 2623
Qy 2433 TTTCTTGTTCACAAAAAATTTCCCTGTAATCTGAAATATATATATATGATACATATAT 2492
Db 2624 TTTCTTGTTCACAAAAAATTTCCCTGTAATCTGAAATATATATATATGATACATATAT 2693
Qy 2493 ATTTTGGAAAAATGGAGCTATGCTGTAATAAGCAACAGGTGGATCAACCCAGTCTGTACTC 2552
Db 2684 ATTTTGGAAAAATGGAGCTATGCTGTAATAAGCAACAGGTGGATCAACCCAGTCTGTACTC 2743

2553 TCTTAACATCTGCATTGAGAGATCAGTATATCTCTCTCAACAAATGGAGGGAG 2612
 Db TCTTAACATCTGCATTGAGAGATCAGTATATCTCTCTCAACAAATGGAGGGAG 2803
 2613 ATGTAGAAATCCCCCTAGAGAGGAGAAACCAATTTATTCAGTGAATACACATCTCT 2672
 Db ATGTAGAAATCCCCCTAGAGAGGAGAAACCAATTTATTCAGTGAATACACATCTCT 2863
 2673 TGTTCCTTAAAAAGCAAGTGTCTTTGGTGTGGAGGACAAATCCCTAGCACTTTCCAC 2732
 Db TGTTCCTTAAAAAGCAAGTGTCTTTGGTGTGGAGGACAAATCCCTAGCACTTTT-CAC 2922
 2733 GTTGTGCTACTAAGAGATCTCAATATATTAGTCTTTGTCGGAGCCCTTCCATAGTACACCT 2792
 Db GTTGTGCTACTAAGAGATCTCAATATATTAGTCTTTGTCGGAGCCCTTCCATAGTACACCT 2982
 2793 TAGCGCTGAGACTGAGCAGGCTTGGGGTTCAGGTAGGTAGACCTGTTAGGGACAGAGCC 2852
 Db TAGCGCTGAGACTGAGCAGGCTTGGGGTTCAGGTAGGTAGACCTGTTAGGGACAGAGCC 3042
 2853 TAGTGGTAAATCCAGAGATGATCTATCCAAAGCTGATTCACAAACCCAGCTCACC 2912
 Db TAGTGGTAAATCCAGAGATGATCTATCCAAAGCTGATTCACAAACCCAGCTCACC 3102
 2913 TGACAGCCGAGGGACAGAGCATCTCTGTCGAGCGACCATTAGGGGCTTTGCCAAG 2972
 Db TGACAGCCGAGGGACAGAGCATCTCTGTCGAGCGACCATTAGGGGCTTTGCCAAG 3162
 2973 TCTACCTTAGAGAAACCCAGTACTCAGACAGGAAAGTCGGGGCTTTGACNACTACCAT 3032
 Db TCTACCTTAGAGAAACCCAGTACTCAGACAGGAAAGTCGGGGCTTTGACNACTACCAT 3222
 3033 ATCTGGTAGCCCATTTCTAGGCATTTGTAATAGTAGGTAGTACACATTTTCAGA 3092
 Db ATCTGGTAGCCCATTTCTAGGCATTTGTAATAGTAGGTAGTACACATTTTCAGA 3282
 3093 CCAATTCAACTGTCTATGACAAATAATCCGGTGGGCTAGATGGAGATAATTTTTTTT 3152
 Db CCAATTCAACTGTCTATGACAAATAATCCGGTGGGCTAGATGGAGATAATTTTTTTT 3342
 3153 CTTCTCAGCTTTATGAGAGAGGAACTGTCTAGGATTCAGCTGAACCAACAGGAACC 3212
 Db CTTCTCAGCTTTATGAGAGAGGAACTGTCTAGGATTCAGCTGAACCAACAGGAACC 3402
 3213 TGGCAACATCAGCTTTAAGCTAAGTGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3272
 Db TGGCAACATCAGCTTTAAGCTAAGTGGAGGCTAACGAGTCTACCTCCCTCTTTGTA 3462
 3273 AATCAAGAAATGTTTAAATGGAGTGTCAATCTTTAAATAAAGATGAATGGTTTC 3332
 Db AATCAAGAAATGTTTAAATGGAGTGTCAATCTTTAAATAAAGATGAATGGTTTC 3522

RESULT 2

US-09-816-494-3
 ; Sequence 3, Application US/09816494
 ; Patent No. 6664089
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel A.
 ; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
 ; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 10448-030002
 ; CURRENT APPLICATION NUMBER: US/09/816,494
 ; CURRENT FILING DATE: 2001-03-23
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1998
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-816-494-3

Query Match 49.8%; Score 1660; DB 4; Length 1998;
 Best Local Similarity 91.8%; Pred. No. 0;
 Matches 1834; Conservative 0; Mismatches 0; Indels 164; Gaps 1;
 562 ATGGCCCATCAGATGATTGGAACTCAAAATTTGTTACTGAGAGGTTGGTGGCTCTCTGGAA 621
 Db 1 ATGGCCCATCAGATGATTGGAACTCAAAATTTGTTACTGAGAGGTTGGTGGCTCTCTGGAA 60
 622 AGTGGAAACGGAAGAGTGTCTGTAATTTGATAGCGGCCATTTTGTGGAATACAAATACATCC 681
 Db 61 AGTGGAAACGGAAGAGTGTCTGTAATTTGATAGCGGCCATTTTGTGGAATACAAATACATCC 120
 682 CACATTTTGAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGGTTGCAACAG 741
 Db 121 CACATTTTGAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGGTTGCAACAG 180
 742 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAAGGTTGACATTGAT 801
 Db 181 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAAGGTTGACATTGAT 240
 802 TGCAGTCAGAGGTTGTTAGTATCAAGCTCCAGAGATGTTGCTCTCTCTCTCTCTCA 861
 Db 241 TGCAGTCAGAGGTTGTTAGTATCAAGCTCCAGAGATGTTGCTCTCTCTCTCTCTCA 300
 862 GACTGTTTCTCACTGTACTCTCTGGGTAAACTGGAGAGAGGTTCAACTCTCTCTCACCTG 921
 Db 301 GACTGTTTCTCACTGTACTCTCTGGGTAAACTGGAGAGAGGTTCAACTCTCTCTCACCTG 360
 922 CTTGCT----- 926
 361 CTTGCAAGTGGTGTGCTGATCTCTCTGTTGTTCCCTGGCTCTGTGAAGGAAATATCC 420
 927 ----- 926
 421 ACTCTAGTCCCTACCTGATTTCTCAGCTTGTGTTACCTGTTGCCAAATTTGGGCCAAC 480
 927 -----AGAGCTGATG 937
 481 CGAATTTCTCCCAATCTTTATCTTGGCTGCGAGGAGATGCTCTCAACAGAGGCTGATG 540
 938 CAGCAGAAATGGGATGGTATGTTTAAATGCCAGCAATACCTGTCCAAAGGCTGACTTT 997
 541 CAGCAGAAATGGGATGGTATGTTTAAATGCCAGCAATACCTGTCCAAAGGCTGACTTT 600
 998 ATCCCGAGTCTCATTTCTCTGCTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 1057
 601 ATCCCGAGTCTCATTTCTCTGCTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660
 1058 CCGTGGTGGACAAATCAGTAGATTTTCAATTTGAGAAAGCAAAAGCTTCAATGGATGTGT 1117
 661 CCGTGGTGGACAAATCAGTAGATTTTCAATTTGAGAAAGCAAAAGCTTCAATGGATGTGT 720
 1118 CTAGTGCACTGTTTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATG 1177
 721 CTAGTGCACTGTTTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATG 780
 1178 AAGAGGATGGACATGTCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAGAGCCTACT 1237
 781 AAGAGGATGGACATGTCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAGAGCCTACT 840
 1238 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTCTGAGCTATGAGAGAGATTAAGAAC 1297
 841 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTCTGAGCTATGAGAGAGATTAAGAAC 900
 1298 CAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGGAGAGGCCAAT 1357
 901 CAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGGAGAGGCCAAT 960
 1358 GAACCTGTCTGCTCTCAGAGGTTGACAGAAAGGAGAGCGCCCTCTAGTCCACCC 1417
 961 GAACCTGTCTGCTCTCAGAGGTTGACAGAAAGGAGAGCGCCCTCTAGTCCACCC 1020


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; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RTS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2377
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (135)...(2012)
; US-09-920-668-3

Query Match      6.8%; Score 225.2; DB 4; Length 2377;
Best Local Similarity 60.6%; Pred. No. 7.7e-60;
Matches 418; Conservative 0; Mismatches 248; Indels 24; Gaps 2;

2y  927 AGGAGCTGATGACGAGCAGATGGGATGGTATGTATGTTAAATGCCAGCAATACCTGTCCAA 986
2b  670 AGGATCTGATGACGCGCAAAATGGAAATAGCTACGTCTCAACGCCAGCAACTCTCTGCCCA 729
2y  987 AGGCTGACTTTATCCCGGAGTCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGTG 1046
2b  730 AGGCTGACTTTCACTCGGAGAGCGGCTTTCATGGGGTCCCCATCAACGCACTACTGTG 789
2y  1047 AGAAATTTTGGCGGTGTGGCAAAATCATAGTATGTTTATGAGAAAGCAAAAGCCTCCA 1106
2b  790 AAAAATCTGTCGCGCTGGCTGGCAAGTCCATCGAGTTTCATGATCAATGAAGCCAGCTCTCA 849
2y  1107 ATGATGTGTCTAGTGCACATGTTAGCTGGGATCTCCGCTCCGCCACCATCGCTATCG 1166
2b  850 GCTGCCAAGTCATCTGCCATCTGCTGGCTGGCATCTCCGCTCTGCCACCATCGCCATCG 909
2y  1167 CCTACATCATGAAGAGATGGACATCTCTTTAGATGAAGCTTTACAGATTTGTGAAGAAA 1226
2b  910 CCTACATCATGAAGACCATGGCATGTCTCCGACGACGCGCTACAGGTTCTGTGAAGGACA 969
2y  1227 AAAGACTACTATATCTCCAACTTCATTTCTGGGCCAACTCTCTGACATATGAGAAGA 1286
2b  970 GCGGCCCGTCCATCTCGCCCACTTCACCTTCTCTGGGCCAGCTGTCTGGAGTACGAGCGCA 1029
2y  1287 AGATTAAAGAACCACTGAGCATGAGGCGCAAGAGCAAACTCAAGCTGCTGACCTGG 1346
2b  1030 CGCTGAGCTGTGCGCGCCCTGACGGGCGACCCGGGACCCCTCAGGAGC---CCGG 1086
2y  1347 AGAAGCCAAATGAACCTGTCCCTGTGTCTGACAGGGTGGACAGAAAGCGAGAGCGCCCC 1406
2b  1087 AGCCTCGCCCACTCTGTGCGCGGGGCGCCGCTGCCACGGCTGCCACCATCTACTCAG 1146
2y  1407 TCAGTCCACCTGTGCGGACTCTGTCTACCTCAGAGGACGACGAGCAAAAGGCCGCTGATC 1466
2b  1147 AGAGCGCTGCGCACAGGAATGCGGCTGCCAGGAGGGCG----- 1185
2y  1467 CCGCCAGCGTSCCAGCGTCCCGAGGTGCGAGCGCTGTCTGTAGAGGACAGCCGCGTGG 1526
2b  1186 GCCTGAGCGGGGCGGGAGCCCCCGCGGCCCCACGCCCCCGGCGACGAGCGCACTGC 1245
2y  1527 TAGAGGGCTCAGTGGGTCTCATCTGCCAGACAGGCTGGAGACAGCAGCANTAGCTCA 1586
2b  1246 AGCAGGGCTGCGCGGCTGCACTCTCTCTCGACCGGCTGAGGACACTAAACCCCTCA 1305
2y  1587 AGGCTCTCTCTCTCTGATATCAAAATCAG 1616
2b  1306 AGCGCTCTCTCTCTCTGGACATCAAGTCTG 1335

RESULT 5
; Sequence 1, Application US/09557921

```

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; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-557-921-1

Query Match      3.3%; Score 109.6; DB 4; Length 1830;
Best Local Similarity 61.0%; Pred. No. 1.7e-23;
Matches 178; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Qy  1006 GTCTCATTTCTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTGGCGTGGT 1065
Db  1187 GTTCAACTAAAGCGCTGCCAGCCACTGACAGCAACAAAGCAGAACCTGCGGCACTTT 1246
Qy  1066 GGAACAATCAGTAGATTTTCATTGAGAAAGCAAAAGCCTCCAAATGGATGTCTTAGTGA 1125
Db  1247 TGAAGAGGCTTTTGTAGTTTCATTGAGGAAGCTCACCAAGTGGGAAGGGCTTCTCATCA 1306
Qy  1126 CTGTTAGTGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGAT 1185
Db  1307 CTGCCAGGCTGGGGTGTCCGCTCCGCCACCATCGCTATCTGCTGATGAAGCACAC 1366
Qy  1186 GGCATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAGACCTACTATATCTTCC 1245
Db  1367 TCGATGACCATGACTGATGCTTATAATTTGTCAAGGCAACGACCAATTAICTCCCC 1426
Qy  1246 AAATTTCAATTTCTGGGCCAACTCTGAGCTATGAGAAAGATTAAGAAC 1297
Db  1427 AAACCTTAATTTCTGGGGCAGTTGCTAGTTCGAGGAGACCTTAAACAAC 1478

RESULT 6
; US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RTS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 2303
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (114)...(1268)
; US-09-922-146-3

Query Match      2.9%; Score 95; DB 4; Length 2303;
Best Local Similarity 58.8%; Pred. No. 8.1e-19;
Matches 164; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy  1004 GAGTCTCATTTCTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTGGCGTGG 1063
Db  858 GACTTTCACTACAAGCAGATCCCATCTCCGACCACTGAGCCAGAACCTGTGCGGTTTC 917
Qy  1064 TTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCCTCCAAATGGATGTCTTAGTG 1123
Db  918 TTTCGAGGACCAATTGAGTTTCATTGATGAGGCTTTGTCCCAAGACTGCGGGGTCTCGTC 977

```

QY 1124 CACTGTTAGCTGGAGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGG 1183
|||
Db 978 CACTGTTGGCGGGGTGAGCGGTTCTGTCAACCGTCACTGTGGCTACCTCATGCAGAAG 1037
|||
QY 1184 ATGGACATGCTTTAGATGAAGCTTACAGATTGTTGGAAGAAAGAAAGACCTACTATATCT 1243
|||
Db 1038 CTCCACCTCTCTCAACGATGCTATGACCTGTCAAGAGGAAGAGTCTACATCTCC 1097
|||
QY 1244 CCAAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAG 1282
|||
Db 1098 CCAAACTTCAATTTCTGGGCCAGTGTGTGGACTTTGAG 1136
|||

RESULT 7

US-09-023-655-347
; Sequence 347, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYNOT03
; CLONE: 1444245
US-09-023-655-347

Query Match 2.8%; Score 94.6; DB 4; Length 1208;
Best Local Similarity 64.3%; Pred. No. 6.6e-19;
Matches 142; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1077 TAGATTTTCAATGAGAAGCAAAAGCCTCCAAATGGATGTTTCTAGTGCACCTGTTTAGCTG 1136
|||
Db 4 TTGAGTTCATTGAGGAAGCTCACCAGTGTGGGAAGGGCTTCTCATCCACTGCCAGGCTG 63
|||
QY 1137 GGAATCTCCCGCTCCGCCACCATCGCTATCGCTATCATGAGGAAGGATGGAATGCTTT 1196
|||

Db 64 GGGTGTCCGCTCCGCCACCATCGTCTACTTGTATGAAGCACACTCGGATGACCA 123
|||
QY 1197 TAGATGAAGCTTACAGATTGTTGAAAGAAAAGACCTACTATATCTCCAAATTCATTT 1256
|||
Db 124 TGACTGATGCTTTATAAATTTGTCAAAGGCAAGACCAATTTATCTCCCAACCTTAAT 183
|||
QY 1257 TTCTGGGGCAACTCCTCGACTATGAGAAGAAAGATTAGAAC 1297
|||
Db 184 TCATGGGCGAGTTGCTAGAGTTTCGAGGAAGACCTAAACAAC 224
|||

RESULT 8

US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1418933
US-09-016-434-1135

Query Match 2.7%; Score 90.2; DB 4; Length 2109;
Best Local Similarity 57.1%; Pred. No. 2.5e-17;
Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 1004 GAGTCTCATTTCTCGGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTCCCGTGG 1063
|||
Db 1105 GAGTTTAATATCAAGCAATCCCATCTCGGATCACTGGAGCAAAACCTGTCCCACTTT 1164
|||
QY 1064 TTGGCAAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCCTCCAATGGAATGTTTCTAGTG 1123
|||
Db 1165 TTCCCTGAGGCCATTTCTTTTCATAGATGAAGCCCGGGGCAAGAACTGTGGTGTCTTGSTA 1224
|||
QY 1124 CACTGTTAGTGGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGG 1183
|||

Db 1225 CATTGCTTGGCTGGCATTAGCCGCTCAGTCACTGTGACTGTGGCTTACCTTATGCGAAG 1284
QY 1184 ATGACATGCTTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTACTATATCT 1243
Db 1285 CTCAATCTGTGATGAACGATGCCTATGACATTGTCAAAATGAAAAATCCAAATATCC 1344
QY 1244 CCAAACTTCAATTTCTGGGCAACTCTCTGGACTATGAGAAAGAT 1290
Db 1345 CCTAACTTCACTTCAUGGTCAGTCTGACTTCGAGAGGAGCT.1391

RESULT 9

US-09-023-655-946
; Sequence 946, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 946:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 91418933
US-09-023-655-946

Query Match 2.7%; Score 90.2; DB 4; Length 2109;
Best Local Similarity 57.1%; Pred. No. 2.5e-17;
Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
QY 1004 GAGTCTCATTTCTCGGTGTCCTGTGTAATGACAGCTTTTGTGAGAAAAATTTTGGCGTGG 1063
Db 1105 GAGTTTAAATACAAAGCAATCCCATCTCGATCACTGGAGCCAAACCTGTCCCAAGTTT 1164
QY 1064 TTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCCCTCCCAATGGATGTCTTAGTG 1123
Db 1165 TTCCTGAGGCCATTCTTTTCATAGATGAAGCCGGGCAAGAACTGTGGTGTCTTGGTA 1224
QY 1124 CACTGTTTAGTGGGATCTCCCGCTCCGCCACCACCTATCGCTATCGCTATCATGAAGAGG 1183

Db 1225 CATTGCTTGGCTGGCATTAGCCGCTCAGTCACTGTGACTGTGGCTTACCTTATGCGAAG 1284
QY 1184 ATGACATGCTTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTACTATATCT 1243
Db 1285 CTCAATCTGTGATGAACGATGCCTATGACATTGTCAAAATGAAAAATCCAAATATCC 1344
QY 1244 CCAAACTTCAATTTCTGGGCAACTCTCTGGACTATGAGAAAGAT 1290
Db 1345 CCTAACTTCACTTCAUGGTCAGTCTGACTTCGAGAGGAGCT.1391

RESULT 10

US-09-016-434-776
; Sequence 776, Application US/09016434
; Patent No. 650938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 776:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVREBCT01
; CLONE: 480457
US-09-016-434-776

Query Match 2.6%; Score 86.2; DB 4; Length 240;
Best Local Similarity 66.5%; Pred. No. 8.5e-17;
Matches 121; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 1116 TTCTAGTGCATCTTTTAGTGGGATCTCCGCTCCGCCACCATCGCTATCGGCTCATCA 1175
Db 10 TTCTCATCCACTCCAGGCTGGGGTGTCCGCTCCGNCACCATCGTCACTGCTTACTTGA 69
QY 1176 TGAAGAGGATGGACATGCTTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTTA 1235
Db 70 TGAAGCACANTCGGATGACCATGACTGCTTATATAATTTGTCAAAGGCAACACCCAA 129
QY 1236 CTATATCTCAAACTTCAATTTTCTGGGCCAACTCTCTGGACTATGAGAAAGAGATTAAGA 1295


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Db 130 TTAATNCCAAACCTTAACCTTCATGGGCGAGTTGCTAGAGTTGAGAGACCTAAACA 189
QY 1296 AC 1297
Db 190 AC 191

RESULT 11
US-09-702-705-801
; Sequence 801, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Lique
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-801

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 993 ACTTTATCCCGAGTCTCATTTCTCGCGTGTGCTGTAATGACAGAGCTTTTGTGAGAAAA 1052
Db 429 ACTTTGAAGGACATATCAGTCAAGTGCATCCAGTGAAGATACACAGGCCGACA 488
QY 1053 TTTTGGCGTGTGGACAAATCAGTAGATTTCATTGAGAAAGCAGAAAGCTTCAATGGAT 1112
Db 489 TCAGTCTCTGTTTATGGAAGCCATAGATACATCGATGCCGTGAGGACTGCCGTGGC 548
QY 1113 GTGTTCTAGTGCACTTTTAGTGGATCTCCGCTCCGCCACCATCGCTATCGCTTACA 1172
Db 549 GCGTCTGTGTCACCTGCCAGCGGGCATCTCGCGTGGCCACCATCTGCTGGCTTACC 608
QY 1173 TCATGAAGAGATGACATGTCTTTAGATGAGATTTGATGAGAAAGAAAGAC 1232
Db 609 TGATGATGAAGAAACGGGTGAGGCTGAGGAGGCGCTTCGAGTTCGTTAAGCAGCGCGCA 668
QY 1233 CTACTATCTCCAACTTCAATTTCTGGGCACTCTGAGTATGAGAGAGATTA 1292
Db 669 GCATTATCTGCGCCAACTTCAGCTTCATGGGCGAGCTGCTGAGTCCAGTCCAGGTGC 728
QY 1293 AGAACGAGACTGGAGCATCAGGCGCCAAAGAC 1324
Db 729 TGCCACGTCCTGTGTCGGAGGCTGTAGC 760

RESULT 12
US-09-736-457-801
; Sequence 801, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
```

```
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Lique
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-801

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 993 ACTTTATCCCGAGTCTCATTTCTCGCGTGTGCTGTAATGACAGCTTTTGTGAGAAAA 1052
Db 429 ACTTTGAAGGACATATCAGTCAAGTGCATCCAGTGAAGATACACAGGCCGACA 488
QY 1053 TTTTGGCGTGTGGACAAATCAGTAGATTTCATTGAGAAAGCAGAAAGCTTCAATGGAT 1112
Db 489 TCAGTCTCTGTTTATGGAAGCCATAGATACATCGATGCCGTGAGGACTGCCGTGGC 548
QY 1113 GTGTTCTAGTGCACTTTTAGTGGATCTCCGCTCCGCCACCATCGCTATCGCTTACA 1172
Db 549 GCGTCTGTGTCACCTGCCAGCGGGCATCTCGCGTGGCCACCATCTGCTGGCTTACC 608
QY 1173 TCATGAAGAGATGACATGTCTTTAGATGAGATTTGATGAGAAAGAAAGAC 1232
Db 609 TGATGATGAAGAAACGGGTGAGGCTGAGGAGGCGCTTCGAGTTCGTTAAGCAGCGCGCA 668
QY 1233 CTACTATCTCCAACTTCAATTTCTGGGCACTCTGAGTATGAGAGAGATTA 1292
Db 669 GCATTATCTGCGCCAACTTCAGCTTCATGGGCGAGCTGCTGAGTCCAGTCCAGGTGC 728
QY 1293 AGAACGAGACTGGAGCATCAGGCGCCAAAGAC 1324
Db 729 TGCCACGTCCTGTGTCGGAGGCTGTAGC 760

RESULT 13
US-09-614-124B-801
; Sequence 801, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-801
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Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 993 ACTTTATCCCCGAGTCTCATTTCTCGCTGTGCTGTGAATGACAGCTTTTGTGAGAAA 1052
DB 429 ACTTTGAGGACACTATCAGTACAAAGTGCATCCAGTGGAGATACCAACAGCCGCA 488

QY 1053 TTTTCCCTGTGTGGCAAAATCAGTAGATTTTCATGTAGAAAGCAAGCCCTCAATGGAT 1112
DB 489 TCAGCTCTCTGTTTCATGGAAGCCATAGATACATCGATGCGTGAAGGACTGCGGTGGC 548

QY 1113 GTGTTCTAGTCACTGTTTACTGCGATCTCCCGCTCGCCACCATCGCTATCGCCTACA 1172
DB 549 GCGTCTCTGTGCTATGCGAGGGGCACTCTCGGTCGGCCACCACTGCTGCGCTTACC 608

QY 1173 TCATGAAGAGATGACATGCTTTTAGTAGAAGCTTACAGATTTGTGAAGAAAAGAC 1232
DB 609 TCATGATGAAGAAACGGGTGAGGCTGCGGTCGGCCACCACTGCTGCGCTTACC 668

QY 1233 CTACTATATCTCCAACTTCAATTTCTGGCCAACTCTCTGGACTATGAGAAAGATTA 1292
DB 669 GCATTATCTGCCCACTTTCAGCTTTCATGGGCGAGCTGCTGCAGTTTCGAGTCCCAAGTGC 728

QY 1293 AGAACCAAGCTGGAGCATCAGGCGCAAGAGC 1324
DB 729 TGGCCACGCTCTGTGCTGCGGAGGCTGCTAGC 760

RESULT 14
US-09-671-325-801
; Sequence 801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671.325
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-801

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 993 ACTTTATCCCCGAGTCTCATTTCTCGCTGTGCTGTGAATGACAGCTTTTGTGAGAAA 1052
DB 429 ACTTTGAGGACACTATCAGTACAAAGTGCATCCAGTGGAGATACCAACAGCCGCA 488

QY 1053 TTTTCCCTGTGTGGCAAAATCAGTAGATTTTCATGTAGAAAGCAAGCCCTCAATGGAT 1112
DB 489 TCAGCTCTCTGTTTCATGGAAGCCATAGATACATCGATGCGTGAAGGACTGCGGTGGC 548

QY 1113 GTGTTCTAGTCACTGTTTACTGCGATCTCCCGCTCGCCACCATCGCTATCGCCTACA 1172
DB 549 GCGTCTCTGTGCTATGCGAGGGGCACTCTCGGTCGGCCACCACTGCTGCGCTTACC 608

QY 1173 TCATGAAGAGATGGRACATGCTTTTAGTAGAAGCTTACAGATTTGTGAAGAAAAGAC 1232
DB 609 TGATGATGAAGAAACGGGTGAGGCTGAGGAGGCGCTTCGAGTTTCGTTAAGCAGCGCCGA 668

QY 1233 CTACTATATCTCCAACTTCAATTTCTGGCCAACTCTCTGGACTATGAGAAAGATTA 1292
DB 669 GCATTATCTGCCCACTTTCAGCTTTCATGGGCGAGCTGCTGCAGTTTCGAGTCCCAAGTGC 728

QY 1293 AGAACCAAGCTGGAGCATCAGGCGCAAGAGC 1324
DB 729 TGGCCACGCTCTGTGCTGCGGAGGCTGCTAGC 760

RESULT 15
US-09-589-184-801
; Sequence 801, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-801

Query Match 2.6%; Score 85.6; DB 4; Length 1619;
Best Local Similarity 53.6%; Pred. No. 5.7e-16;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 993 ACTTTATCCCCGAGTCTCATTTCTCGCTGTGCTGTGAATGACAGCTTTTGTGAGAAA 1052
DB 429 ACTTTGAGGACACTATCAGTACAAAGTGCATCCAGTGGAGATACCAACAGCGCGCA 488

QY 1053 TTTTCCCTGTGTGGCAAAATCAGTAGATTTTCATGTAGAAAGCAAGCCCTCAATGGAT 1112
DB 489 TCAGCTCTCTGTTTCATGGAAGCCATAGATACATCGATGCGTGAAGGACTGCGGTGGC 548

QY 1113 GTGTTCTAGTCACTGTTTACTGCGATCTCCCGCTCGCCACCATCGCTATCGCCTACA 1172
DB 549 GCGTCTCTGTGCTATGCGAGGGGCACTCTCGGTCGGCCACCACTGCTGCGCTTACC 608

QY 1173 TCATGAAGAGATGGRACATGCTTTTAGTAGAAGCTTACAGATTTGTGAAGAAAAGAC 1232
DB 609 TGATGATGAAGAAACGGGTGAGGCTGAGGAGGCGCTTCGAGTTTCGTTAAGCAGCGCCGA 668

QY 1233 CTACTATATCTCCAACTTCAATTTCTGGCCAACTCTCTGGACTATGAGAAAGATTA 1292
DB 669 GCATTATCTGCCCACTTTCAGCTTTCATGGGCGAGCTGCTGCAGTTTCGAGTCCCAAGTGC 728

QY 1293 AGAACCAAGCTGGAGCATCAGGCGCAAGAGC 1324
DB 729 TGGCCACGCTCTGTGCTGCGGAGGCTGCTAGC 760

Search completed: February 28, 2004, 00:57:49
Job time : 227 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	3332	100.0	3332	9	US-09-964-277-20	Sequence 20, Appl
2	3158	94.8	3495	9	US-09-964-277-1	Sequence 1, Appli
3	3145	94.4	3625	12	US-10-425-114-26234	Sequence 26234, A
4	2350	88.5	3544	9	US-09-816-494-1	Sequence 1, Appli
5	2950	88.5	3544	15	US-10-377-073-25	Sequence 25, Appl
6	1795.4	53.9	1916	15	US-10-108-260A-2429	Sequence 2429, Ap
7	1762.4	52.9	2102	15	US-10-094-749-673	Sequence 673, App
8	1742	52.3	2200	12	US-10-072-013-255	Sequence 255, App
9	1712.4	51.4	2071	12	US-10-072-013-257	Sequence 257, App
10	1560	49.8	1998	9	US-09-816-494-3	Sequence 3, Appli
11	1860	49.8	1998	15	US-10-377-073-27	Sequence 27, Appl
12	886.8	26.6	2558	15	US-10-104-047-1750	Sequence 1750, Ap
13	595	17.9	787	15	US-10-220-891-85	Sequence 85, Appl
14	537.4	16.1	878	9	US-09-764-853-158	Sequence 158, App
15	409.2	12.3	478	10	US-09-918-993-25801	Sequence 25801, A

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Db 2881 ATCCAAAGCTGATTCACAAAACCCAGCTGACCTGACAGCCGAGGACACGAGCATCCTC 2940
Qy 2941 TGCTGGACGACCAATAGGCGCTTGCAGAGCTTACCTTAGAGCAAAACCGAGTCTCA 3000
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Db 3001 GACAGGAAGTCGGGCTTTGACCACTACCATATCTGTTAGCCCATTTTCTAGGCAATCT 3060
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Qy 3181 CTGTCTAGGATTCAGCTGAACCAACAGGAACTGGCAACATCAGATTTTAAAGCTAAGTT 3240
Db 3181 CTGTCTAGGATTCAGCTGAACCAACAGGAACTGGCAACATCAGATTTTAAAGCTAAGTT 3240
Qy 3241 GGGAGGCTAACGAGTCTACCTCCCTCTTTGTAATCAAGAAATGTTAAATGGGATTTG 3300
Db 3241 GGGAGGCTAACGAGTCTACCTCCCTCTTTGTAATCAAGAAATGTTAAATGGGATTTG 3300
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RESULT 2

US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434

; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Query Match

Best Local Similarity 94.8%; Score 3158; DB 9; Length 3496;
Matches 3332; Conservative 0; Mismatches 0; Indels 164; Gaps 1;

Qy 1 GAGAGAGGAGAGATATATATCTGAAAGACAGAGAGGAGCGGACCGGACCGGAC 60
Db 1 GAGAGAGGAGAGATATATATCTGAAAGAGAGAGGAGGAGGAGCGGACCGGAC 60
Qy 61 GCGAGCGGAGCGCAGCGCCCTCTCGGCTCCGCGCGCGGCTCCCAAGTCCGGAGGC 120
Db 61 GCGAGCGGAGCGCAGCGCCCTCTCGGCTCCGCGCGCGGCTCCCAAGTCCGGAGGC 120
Qy 121 GAGGGGGCCCGAGGGGAGAGCGCCGTGACAACTTTCGTTTCCCTCTGAGGAAATGGGAG 180
Db 121 GAGGGGGCCCGAGGGGAGAGCGCCGTGACAACTTTCGTTTCCCTCTGAGGAAATGGGAG 180
Qy 181 GTCGGCGGCCCAAAAAGCTTTCAGTCCAGTGTAAAGCTGTGAGCGCGGAGCAAAAGCT 240
Db 181 GTCGGCGGCCCAAAAAGCTTTCAGTCCAGTGTAAAGCTGTGAGCGCGGAGCAAAAGCT 240
Qy 241 AAAGAATGATGTAATCGGCTGGCTCTCCAAAGCATCTTTTGTGFGAATGGTTATCC 300
Db 241 AAAGAATGATGTAATCGGCTGGCTCTCCAAAGCATCTTTTGTGFGAATGGTTATCC 300
Qy 301 AGTCATCTCTTATGATCAAAATGTGAGGGGCTGCTTGTGAGCGAGTCTTTCGCAAG 360
Db 301 AGTCATCTCTTATGATCAAAATGTGAGGGGCTGCTTGTGAGCGAGTCTTTCGCAAG 360
Qy 361 GCACATCAACGGGAAAGAGAAAGAGACATTCACCTGGAGGGCTCTTGTGAAAAATGGGTT 420
Db 361 GCACATCAACGGGAAAGAGAAAGAGACATTCACCTGGAGGGCTCTTGTGAAAAATGGGTT 420
Qy 421 TAACTCTCTTTTCCGAGTCAACCAAGCTGACCTCATACATTTTAGTCAATGGAGT 480
Db 421 TAACTCTCTTTTCCGAGTCAACCAAGCTGACCTCATACATTTTAGTCAATGGAGT 480
Qy 481 GGCTGAGCCTTTGAGCACAACCACTTATCATCTGTCGCAAAATTAAGAGAGAGTGG 540
Db 481 GGCTGAGCCTTTGAGCACAACCACTTATCATCTGTCGCAAAATTAAGAGAGAGTGG 540
Qy 541 AAAAGAGGACTTATTTGTCATGGCCCATGAGATGATTTGAACTCAAAATTTTACTGAG 600
Db 541 AAAAGAGGACTTATTTGTCATGGCCCATGAGATGATTTGAACTCAAAATTTTACTGAG 600
Qy 601 AGTTTGTGCTCTGCTGGAAAGTGGAAACGAAAAAGTCTGCTAATTCATAGCCGCCA 660
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Qy 661 TTTTGGAAATACATATACATCCCATTTTGGAGCCATTAATATCAATCTGCTCCAGCTT 720
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Qy 721 ATGAGCGGAGGTTGCAACAGGACAAAGTGTAAATTAACAGAGCTCATCCAGATTCAGG 780
Db 721 ATGAGCGGAGGTTGCAACAGGACAAAGTGTAAATTAACAGAGCTCATCCAGATTCAGG 780
Qy 781 AAACATAAGCTTGACATTTGATTCAGTCAAGAGTTTGTAGTTTACGATCAAAAGCTCCCAA 840
Db 781 AAACATAAGCTTGACATTTGATTCAGTCAAGAGTTTGTAGTTTACGATCAAAAGCTCCCAA 840
Qy 841 GATGTTGCTCTCTCTTCAGACTGTTTTCTCAGTGTACTTCTGGTAACTGGAGAG 900
Db 841 GATGTTGCTCTCTCTTCAGACTGTTTTCTCAGTGTACTTCTGGTAACTGGAGAG 900

QY	901	AGCTTCAA	CTGTTCAC	TGCTTGC	-----	926
Db	901	AGCTTCAA	CTGTTCAC	TGCTTGC	AGGTTGCTGAGTTCTCTCGTTGTTCCCT	960
QY	927	-----	-----	-----	-----	926
Db	961	GGCTCTCT	GTGAAGAA	AAATCCACT	GTAGTCCCTACTCGCAITTTCTCAGCCTTGCTTACCT	1020
QY	927	-----	-----	-----	-----	926
Db	1021	GTTCGCAAC	ATTGGGCA	ACCGGAATTC	TTCCCAATCTTTATCTTTGGCTGCCAGCAGAT	1080
QY	927	-----	-----	-----	-----	926
Db	1081	GTTCCTCAA	CAGGAGCT	GTATGACGAGA	ATGGGATTGGTTATGTCTTAAATGCCAGCAAT	1140
QY	977	ACCTGTCCAA	AGCCTGACT	TTATCCCGAGT	CTCTATTTCCCTCGTGTGCCCTGTCAATGAC	1036
Db	1141	ACCTGTCCAA	AGCCTGACT	TTATCCCGAGT	CTCTATTTCCCTCGTGTGCCCTGTCAATGAC	1200
QY	1037	AGCTTTTGT	GAGAAAAT	TTTTCGCGT	GGTTGGACAAATCAGTAGATTTCAATGAGAAAGCA	1096
Db	1201	AGCTTTTGT	GAGAAAAT	TTTTCGCGT	GGTTGGACAAATCAGTAGATTTCAATGAGAAAGCA	1260
QY	1097	AAAGCCTCCA	ATGGATGT	CTCTAGTGCA	CTGTTAGCTGGGATCTCCCGTCCGCCACC	1156
Db	1261	AAAGCCTCCA	ATGGATGT	CTCTAGTGCA	CTGTTAGCTGGGATCTCCCGTCCGCCACC	1320
QY	1157	ATCGCTAT	TCGCTACAT	CATGAAGAGG	ATGGACATGTTTAGATGAAGCTTACAGATTT	1216
Db	1321	ATCGCTAT	TCGCTACAT	CATGAAGAGG	ATGGACATGTTTAGATGAAGCTTACAGATTT	1380
QY	1217	GTGAAGAAA	AAAGACCT	ACTATATCT	CCAACTTCAATTTCTGGGCGAATCCTCGAC	1276
Db	1381	GTGAAGAAA	AAAGACCT	ACTATATCT	CCAACTTCAATTTCTGGGCGAATCCTCGAC	1440
QY	1277	TATGAGAAA	GAGATTAA	GAAACCA	CTGAGCATCAGGCGCAAGAGCAAACTCAAGCTG	1336
Db	1441	TATGAGAAA	GAGATTAA	GAAACCA	CTGAGCATCAGGCGCAAGAGCAAACTCAAGCTG	1500
QY	1337	CTGCACTTG	GAGAGCCAA	TGTAACCTG	TCTCTGCTGTCTCAGAGGGTGGACAGAAAGC	1396
Db	1501	CTGCACTTG	GAGAGCCAA	TGTAACCTG	TCTCTGCTGTCTCAGAGGGTGGACAGAAAGC	1560
QY	1397	GAGACGCC	CCCTCAGT	CCACCTGTG	CCGACTCTGTACTCTCAGAGCGCAGCAGGCAAGG	1456
Db	1561	GAGACGCC	CCCTCAGT	CCACCTGTG	CCGACTCTGTACTCTCAGAGCGCAGCAGGCAAGG	1620
QY	1457	CCCGTGCA	TCCCGCAG	CGTCCCGAG	CGTCCCGAGCGTCCAGCGCTCGCTGTAGAGAC	1516
Db	1621	CCCGTGCA	TCCCGCAG	CGTCCCGAG	CGTCCCGAGCGTCCAGCGCTCGCTGTAGAGAC	1680
QY	1517	AGCCCGCT	GTGTACAG	GGCGCTCAGT	GGCGTGCACCTGTCCGACAGACAGCTGGAGACAGC	1576
Db	1681	AGCCCGCT	GTGTACAG	GGCGCTCAGT	GGCGTGCACCTGTCCGACAGACAGCTGGAGACAGC	1740
QY	1577	AATAAGCT	CAAGCGTCC	TCTCTCGAT	CAAAATCAGTTTTCATTTACGACGACGATG	1636
Db	1741	AATAAGCT	CAAGCGTCC	TCTCTCGAT	CAAAATCAGTTTTCATTTACGACGACGATG	1800
QY	1637	GCAGCATCT	TACATATG	GGTTCTCTCAT	ACAGATGCTTTGGATATCTACAAACCTTCC	1696
Db	1801	GCAGCATCT	TACATATG	GGTTCTCTCAT	ACAGATGCTTTGGATATCTACAAACCTTCC	1860
QY	1697	ACTACTCT	GGATGGAG	CCAAACAG	CTATGCCAGTTCTCCCTGTTCAGAACTATCGGAG	1756
Db	1861	ACTACTCT	GGATGGAG	CCAAACAG	CTATGCCAGTTCTCCCTGTTCAGAACTATCGGAG	1820
QY	1757	CAGACTCT	CCGAAAAC	AGTCTGTGA	TAGGAGGAAAGCCAGCATCCCCAAGAGCTCGAGAC	1816
Db	1921	CAGACTCT	CCGAAAAC	AGTCTGTGA	TAGGAGGAAAGCCAGCATCCCCAAGAGCTCGAGAC	1980

1817	QY	GCCAGGCGTTTCAGACAGACCGAGAGCAAGCGATTGCAATTCGGTTCAGAAACGACGACGAGTGGC	1876
1981	DB	GCCAGGCGTTTCAGACAGACCGAGAGCAAGCGATTGCAATTCGGTTCAGAAACGACGACGAGTGGC	2040
1877	QY	ACCCGCCAGAGGTCCTTTTATCTCCACATGCATCGAAGTGGGAGCGTGGAGGACAAATTAC	1936
2041	DB	ACCCGCCAGAGGTCCTTTTATCTCCACATGCATCGAAGTGGGAGCGTGGAGGACAAATTAC	2100
1937	QY	CACACCGAGCTTCCTTTTCGGCCTTTCCACCGACGACGACACCTCAGAAAGTCGTGGTC	1996
2101	DB	CACACCGAGCTTCCTTTTCGGCCTTTCCACCGACGACGACACCTCAGAAAGTCGTGGTC	2160
1997	QY	CTGGGCGTTAAGGCGTGGCACTCGGATATCTTTGGCCCCCGACAGACTCTACCCCTTCCTCG	2056
2161	DB	CTGGGCGTTAAGGCGTGGCACTCGGATATCTTTGGCCCCCGACAGACTCTACCCCTTCCTCG	2220
2057	QY	ACCAGCAGCTGGTATTTTGGCCACAGAGTCCTCACACTTCTACTCTGGCTCAGCCATCTAC	2116
2221	DB	ACCAGCAGCTGGTATTTTGGCCACAGAGTCCTCACACTTCTACTCTGGCTCAGCCATCTAC	2280
2117	QY	GGAGCGAGTCGAGTTACTCTGCCTACAGCTCGACCGAGCTGCCACTTTGGGAGACCA	2176
2281	DB	GGAGCGAGTCGAGTTACTCTGCCTACAGCTCGACCGAGCTGCCACTTTGGGAGACCA	2340
2177	QY	GTCATTCTGTGCGCAGCGGCGAGAAAGCAAGTGACAGAGCTGACTCGCGCGGAGCTGG	2236
2341	DB	GTCATTCTGTGCGCAGCGGCGAGAAAGCAAGTGACAGAGCTGACTCGCGCGGAGCTGG	2400
2237	QY	CATGAAGAGAGCCCTTTGAAAGCAGTTTAAACGCGAGAGCTGCGCAATGGAAATTTGGA	2296
2401	DB	CATGAAGAGAGCCCTTTGAAAGCAGTTTAAACGCGAGAGCTGCGCAATGGAAATTTGGA	2460
2297	QY	GAGAGCATCATGTTCAGAGAACAGCTCACGGGAAGAGCTGGGGAAGTGGGCGAGTCAGTCT	2356
2461	DB	GAGAGCATCATGTTCAGAGAACAGCTCACGGGAAGAGCTGGGGAAGTGGGCGAGTCAGTCT	2520
2357	QY	AGCTTTTCGGCGCAGTCGGAATTCATTGAGGTCCTCTGAGAAGAAAGACACTTGTGACTT	2416
2521	DB	AGCTTTTCGGCGCAGTCGGAATTCATTGAGGTCCTCTGAGAAGAAAGACACTTGTGACTT	2580
2417	QY	CTATAGACAAATTTTTTTCTGTTCACAAAAAATTCCTGTAAATCTGAAATATATAT	2476
2581	DB	CTATAGACAAATTTTTTTCTGTTCACAAAAAATTCCTGTAAATCTGAAATATATAT	2640
2477	QY	ATGTACATACATATATATTTTTGGAAAAATGGAGCTATGGTGTAAAAAGCAACAGCTGGATC	2536
2641	DB	ATGTACATACATATATATTTTTGGAAAAATGGAGCTATGGTGTAAAAAGCAACAGCTGGATC	2700
2537	QY	AACCCAGTTGTTACTCTCTTAAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAAC	2596
2701	DB	AACCCAGTTGTTACTCTCTTAAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAAC	2760
2597	QY	AAAAATGGAAGGCGAGATGCTAGAAATCCCCCTTCAGACGGAGGAAAAACCATTTTATTCAGT	2656
2761	DB	AAAAATGGAAGGCGAGATGCTAGAAATCCCCCTTCAGACGGAGGAAAAACCATTTTATTCAGT	2820
2657	QY	GAAATTACACATCTCTTTGTTCTTTAAAAAAGCAAGTGTCTTTGGTGTGGAGGACAAAATC	2716
2821	DB	GAAATTACACATCTCTTTGTTCTTTAAAAAAGCAAGTGTCTTTGGTGTGGAGGACAAAATC	2880
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2881	DB	CCCTACCAATTTTCCAGTTGTGCTACTAGAGATCTCAAAATATTAGTCTTTGTCGGACC	2940
2777	QY	CTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTTGGGGGTTCAGGTAGGTAGACCC	2836
2941	DB	CTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTTGGGGGTTCAGGTAGGTAGACCC	3000
2837	QY	TGTTAGGGAAGAGGCTTAGTGTGTAATCCAGAGAAATGATCCCTATCCAAAGCTGATTCA	2896
3001	DB	TGTTAGGGAAGAGGCTTAGTGTGTAATCCAGAGAAATGATCCCTATCCAAAGCTGATTCA	3060
2897	QY	CAAAACCCAGCTCACTGACAGCGGAGGACACGAGCATCACTCTGCTGGAGGAGCCATT	2956

Db 1392 AGCCCTCCAAATGAGTGTCTTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCCACCA 1451
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QY 1938 ACACGAGCTTCTTTTTCGGCTTTCCACAGCCAGCAGCAGCTCAGAGCTCAGAGCTCGGCC 1997
Db 2232 ACACGAGCTTCTTTTTCGGCTTTCCACAGCCAGCAGCAGCTCAGAGCTCAGAGCTCGGCC 2291
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QY 2058 CCAGCAGCTGATTTTGGCCAGAGTCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2117
Db 2352 CCAGCAGCTGATTTTGGCCAGAGTCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2411
QY 2118 GAGCGCTGCGAGTACTCTGCTCAGCTGAGCGCAGCTGCGCCACTTTCGGAGACCAAG 2177
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QY 2238 ATGAAGAGAGCCCTTTGAAAAGCAGTTTAAAACGAGAGCTGCCAAATGGAATTTGGAG 2297
Db 2532 ATGAAGAGAGCCCTTTGAAAAGCAGTTTAAAACGAGAGCTGCCAAATGGAATTTGGAG 2591
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Db 2592 AGAGCATCATGTGAGAGAACAGGTACGGGAAGAGCTGCGGAAGTGGGCGAGTCAGTCTA 2651
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Db 2652 GCTTTTTCGGGAGCATGGAATCATTTGAGGTCTCTGAGAGAAAGACACTTGTGTACTTC 2711
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Db 2772 TGTACATACATATATATTTTTTTGAAAAATGGAGCTATGTTGTAAGCAACAGGTGGATCA 2831
QY 2538 ACCCAGTTTACTCTCTTAACATCTGCATTTGAGAGTCAAGCTATACCTCTCTCAACA 2597
Db 2832 ACCCAGTTTACTCTCTTAACATCTGCATTTGAGAGTCAAGCTATACCTCTCTCAACA 2891
QY 2598 AAAATGGAAGGCGAGATGCTAGAAATCCCTCTAGACGGAGGAAAAACCATTTTATTCAGTG 2657
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QY 2658 AATTAACATCTCTCTGTTTAAAAAAGCAGTGTCTTTGGTGTGGAGGACAAATCC 2717
Db 2952 AATTAACATCTCTCTGTTTAAAAAAGCAGTGTCTTTGGTGTGGAGGACAAATCC 3011
QY 2718 CTTACATTTTCCAGCTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGAGCCC 2777
Db 3012 CTTACATTTT- CAGTTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGAGCCC 3070
QY 2778 TTCCATAGTACACCTTAGCGCTGAGCTGAGCCAGCTTTGGGGTTCAGGTAGTAGCCCT 2837
Db 3071 TTCCATAGTACACCTTAGCGCTGAGCTGAGCCAGCTTTGGGGTTCAGGTAGTAGCCCT 3130
QY 2838 GTTAGGGAAGAGCCTAGTGTAAATCCAGAGAAATGATCCTTATCCAAAGCTGATTAC 2897
Db 3131 GTTAGGGAAGAGCCTAGTGTAAATCCAGAGAAATGATCCTTATCCAAAGCTGATTAC 3190
QY 2898 AAAACCCAGCTCACTCTGACAGCCGAGGAGACACGAGCATCACTGTGTGGACGGACCAATTA 2957
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QY 3198 GAACCAACAGGAACCTGGCAACATCAGATTAAAGCTTAAGTTGGGAGGCTTAACGAGTCT 3257
Db 3491 GAACCAACAGGAACCTGGCAACATCAGATTAAAGCTTAAGTTGGGAGGCTTAACGAGTCT 3550
QY 3258 ACCTCCCTCTTTGTAATAAACAAGAAATTTGTAATAAAGGATTTGTAATAAATAA 3317
Db 3551 ACCTCCCTCTTTGTAATAAACAAGAAATTTGTAATAAAGGATTTGTAATAAATAA 3610

QY 3318 GATGAACCTGGTTTC 3332
Db 3611 GATGAACCTGGTTTC 3625

RESULT 4

US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Query Match 88.5%; Score 2950; DB 9; Length 3544;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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Db 344 ATCAAAATGAGGGGCTGCTTTGTTGGACGAGTCTTTTGAAGACATCAACGGGAAA 403
QY 377 GAGAAAGAGACATTCACCTGGAGGGCTCTTGCTGAAATCGGTTAACTCTCCTTTTGC 436
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QY 437 AGTCACCAACCGCTGACCTCATACATTTTAGTACAAATGGAGTGGCTGAGCCTTTGAGC 496
Db 464 AGTCACCAACCGCTGACCTCATACATTTTAGTACAAATGGAGTGGCTGAGCCTTTGAGC 523
QY 437 ACACCAACATTCATCATCTGTCGCAATTAAGAGAGAGTGGGAAAGAGGACTTATTG 556
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QY 557 TTGTCATGGCCCATGAGATGATTGGAATCAAAATGTTTACTGAGAGGTTGGTGGCTCTGC 616
Db 584 TTGTCATGGCCCATGAGATGATTGGAATCAAAATGTTTACTGAGAGGTTGGTGGCTCTGC 643
QY 617 TGGAAAGTGGAAACGGAAAGTGTGCTAATGATAGCGGCCATTTGTTGGAATACAATA 676
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QY 737 AACAGGACAAAGTGTTAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 796
Db 764 AACAGGACAAAGTGTTAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 823

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QY 917 ACCTGCTTGC----- 926
Db 944 ACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCCTCTGTGAAGGAA 1003
QY 927----- 926
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QY 1233 CTACTATATCTCAAACTTCAATTTTCTGGGCCAACTCTCTGGAATATGAGAAGAGATTA 1292
Db 1424 CTACTATATCTCAAACTTCAATTTTCTGGGCCAACTCTCTGGAATATGAGAAGAGATTA 1483
QY 1293 AGAACAGAGCTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGC 1352
Db 1484 AGAACAGAGCTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGC 1543
QY 1353 CAAATGAACCTGTCCCTGTGCTCTCAGAGGGTGGACAGAAAAAGCGAGACGCCCTCAGTC 1412
Db 1544 CAAATGAACCTGTCCCTGTGCTCTCAGAGGGTGGACAGAAAAAGCGAGACGCCCTCAGTC 1603
QY 1413 CACCTGTGCGGACTGCTTACCTCAGAGGCGAGGACAAAGGCCCGCTGCATCCGCCCA 1472
Db 1604 CACCTGTGCGGACTGCTTACCTCAGAGGCGAGGACAAAGGCCCGCTGCATCCGCCCA 1663
QY 1473 GCGTGCCAGCGTGCCCGAGCGTGCGCTGTGTAGAGGACAGCCCGCTGGTACAGG 1532
Db 1664 GCGTGCCAGCGTGCCCGAGCGTGCGCTGTGTAGAGGACAGCCCGCTGGTACAGG 1723
QY 1533 CGCTCAGTGGGCTGACCTGTCCGAGACAGGCTGGAAGACAGCAATAAGCTCAACGTT 1592
Db 1724 CGCTCAGTGGGCTGACCTGTCCGAGACAGGCTGGAAGACAGCAATAAGCTCAACGTT 1783
QY 1593 CCTTCTCTCTGGATATCAAAATCAGTTTCTATATTCAGCCAGCATGGCAGCATCTTACATG 1652
Db 1784 CCTTCTCTCTGGATATCAAAATCAGTTTCTATATTCAGCCAGCATGGCAGCATCTTACATG 1843
QY 1653 GCTTCTCCTCATCAGAAAGTCTTTGGAATATCTAATAAATCTTCCACTACTCTGGATGGA 1712
Db 1844 GCTTCTCCTCATCAGAAAGTCTTTGGAATATCTAATAAATCTTCCACTACTCTGGATGGA 1903

PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589)...(2586)
US-10-377-072-25

Query Match 88.5%; Score 2950; DB 15; Length 3544;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

197 GCTTTCAAGTCCAGTGTAAAGCTGTTGGAGCGGGAGCAAGGTAAAGAAATGATGTAATG 256
Db GCTTTCAAGTCCAGTGTAAAGCTGTTGGAGCGGGAGCAAGGTAAAGAAATGATGTAATG 283

257 CGCTGGCTGCTCCAAAGCATCTTTGTTGGAATGTTATCCAGTCATCTCTTTATGA 316
Db CGCTGGCTGCTCCAAAGCATCTTTGTTGGAATGTTATCCAGTCATCTCTTTATGA 343

317 ATCAAAATGTAGGGGCTGCTTTGTGACGGAGTCTTTGCAAGAGCACATCAACGGGAAA 376
Db ATCAAAATGTAGGGGCTGCTTTGTGACGGAGTCTTTGTGACAGCACATCAACGGGAAA 403

377 GAGAAAGAGACATTCACCTTGAGGGCTCTGCTGAAATGGTTTAACTCTCTCTTTGCC 436
Db GAGAAAGAGACATTCACCTTGAGGGCTCTGCTGAAATGGTTTAACTCTCTCTTTGCC 463

437 ACTCACCAACGAGCTGACCTCATACACTTTTAGTACAAATGAGTGGCTGAGCCTTTGAGC 496
Db ACTCACCAACGAGCTGACCTCATACACTTTTAGTACAAATGAGTGGCTGAGCCTTTGAGC 523

497 ACACCAACCATTAACATCATCTGTCGCAAAATTAAGAGAGGAGTGGGAAAGAGGACTTATTG 556
Db ACACCAACCATTAACATCATCTGTCGCAAAATTAAGAGAGGAGTGGGAAAGAGGACTTATTG 583

557 TTGTCATGCCCCATGAGATGATGGAATCAAAATGTTACTGAGAGTGGTGGCTCTGC 616
Db TTGTCATGCCCCATGAGATGATGGAATCAAAATGTTACTGAGAGTGGTGGCTCTGC 643

617 TGGAAAGTGGAAACGGAAGAGTGTCTTAATTTGATAGCGGCCAATTTGTGGAATACAATA 676
Db TGGAAAGTGGAAACGGAAGAGTGTCTTAATTTGATAGCGGCCAATTTGTGGAATACAATA 703

677 CATCCACATTTTGAAGCCATTAATATCAACTGCTCCAGCTGTATGAAGCAAGGTTGC 736
Db CATCCACATTTTGAAGCCATTAATATCAACTGCTCCAGCTGTATGAAGCAAGGTTGC 763

737 AACAGGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 796
Db AACAGGACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACA 823

797 TTGAATTCAGTCAAGAGTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCT 856
Db TTGAATTCAGTCAAGAGTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCT 883

857 CTTGAGACTGTTTCTCACTGACTCTCTGGTAACTGGGAGAGAGCTTCAACTCTGTTTC 916
Db CTTGAGACTGTTTCTCACTGACTCTCTGGTAACTGGGAGAGAGCTTCAACTCTGTTTC 943

917 ACCTGCTTGC----- 926
944 ACCTGCTTGCAGGTGGGTTTGTCTGAGTCTCTGTTTCCCTGGCCTCTGTGAAGGAA 1003
927 ----- 926

Db 1004 AATCCACTCTAGTCCCTACCTGCAATTTCTCAGCGCTTGCCTTACCTGTGTCACCAATGGGC 1063
QY 927 -----AGAGC 932

Db 1064 CAACCCGAATTCCTCCCAATCTTTATCTTGGCTGCCAGCGAGATGCTCTCAACAAGGAGC 1123
QY 933 TGATGCAGCAGAATGGGATGTTATGTTTAAATGCAGCAATACCTGTCCAAAGCCTG 992
Db 1124 TGATGCAGCAGAATGGGATGTTATGTTTAAATGCAGCAATACCTGTCCAAAGCCTG 1183

QY 993 ACTTTATCCCGAGTCTCATTTCTGCTGTGCTGTGAATGACAGCTTTTGTGAGAAA 1052
Db 1184 ACTTTATCCCGAGTCTCATTTCTGCTGTGCTGTGAATGACAGCTTTTGTGAGAAA 1243

QY 1053 TTTTGGCGTGTGTCACAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGGAT 1112
Db 1244 TTTTGGCGTGTGTCACAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGGAT 1303

QY 1113 GHGTTCTAGTCACTGTTTGTAGTGGGATCTCCGCTCCGCCACCATCGCTATCGCCTACA 1172
Db 1304 GTGTTCTAGTCACTGTTTGTAGTGGGATCTCCGCTCCGCCACCATCGCTATCGCCTACA 1363

QY 1173 TCATGAAGAGATGGAATGTTTGTAGTGAAGTTACAGATTTGTGAAGAAAGAAC 1232
Db 1364 TCATGAAGAGATGGAATGTTTGTAGTGAAGTTACAGATTTGTGAAGAAAGAAC 1423

QY 1233 CTACTATATCTCCAAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAAGATTA 1292
Db 1424 CTACTATATCTCCAAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAAGATTA 1483

QY 1293 AGAACAGACTGGAGATCGGGCCAAAGAGCAAACTCAAGCTGTGTCACCTGGAGAGC 1352
Db 1484 AGAACAGACTGGAGATCGGGCCAAAGAGCAAACTCAAGCTGTGTCACCTGGAGAGC 1543

QY 1353 CAAATGAACCTGTCCTGCTGTCTCAGAGGTGAGCAAGAAAGCAGAGCCGCTCAGTC 1412
Db 1544 CAAATGAACCTGTCCTGCTGTCTCAGAGGTGAGCAAGAAAGCAGAGCCGCTCAGTC 1603

QY 1413 CACCTGTGCGACTCTGCTACCTCAGAGGACAGGACAAAGCCGCTGTCATCCGCCCA 1472
Db 1604 CACCTGTGCGACTCTGCTACCTCAGAGGACAGGACAAAGCCGCTGTCATCCGCCCA 1663

QY 1473 GCGTGCCAGCGTCCAGCGTGCAGCGCTGCTGTAGAGGACAGCGCGCTGGTACAGG 1532
Db 1664 GCGTGCCAGCGTCCAGCGTGCAGCGCTGCTGTAGAGGACAGCGCGCTGGTACAGG 1723

QY 1533 CGCTCAGTGGGCTGCACCTGTCGCGCAGACAGAGGTGGAAGACAGCAATAAGCTCAAGCGTT 1592
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QY 1593 CTTTCTCTCTGGATATCAAAATCAGTTTTCATATTCAGCGACGATGGCAGCATCTTACATG 1652
Db 1784 CTTTCTCTCTGGATATCAAAATCAGTTTTCATATTCAGCGACGATGGCAGCATCTTACATG 1843

QY 1653 GCTTCTCTCATCAGAAGATGCTTTGGAATCTACAAACCTTCCACTACTCTGATGGGA 1712
Db 1844 GCTTCTCTCATCAGAAGATGCTTTGGAATCTACAAACCTTCCACTACTCTGATGGGA 1903

QY 1713 CCAACAAGCTATGCGAGTCTCCCTGTTTCAAGAAATATCGGAGCAGATCCCGGAAACCA 1772
Db 1904 CCAACAAGCTATGCGAGTCTCCCTGTTTCAAGAAATATCGGAGCAGATCCCGGAAACCA 1963

QY 1773 GTCTGTATAGGGAGAGCCAGCATCCCAAGAGCTGAGACCGCCAGCGCTTCAGACA 1832
Db 1964 GTCTGTATAGGGAGAGCCAGCATCCCAAGAGCTGAGACCGCCAGCGCTTCAGACA 2023

QY 1833 GCCAGACAAGCGATTTGCAATTCGCTCAGAACCCAGCAGCAGTGGCACCGCCAGAGGTCCC 1892
Db 2024 GCCAGACAAGCGATTTGCAATTCGCTCAGAACCCAGCAGCAGTGGCACCGCCAGAGGTCCC 2083

QY 1893 TTTTATCTCACTGCATCGAAGTGGGAGCGTGGAGGACAAATACACACAGCTTCTTT 1952
Db 2084 TTTTATCTCACTGCATCGAAGTGGGAGCGTGGAGGACAAATACACACAGCTTCTTT 2143

QY	1953	TCGGCCTTTCCACGAGCCAGCAGAGCACTCA	CGAAGTCTGCTGGCCTTGAAGGCTT	2012
DB	2144	TCGGCCTTTCCACGAGCCAGCAGCAGCACTC	CACGAAGTCTGCTGGCCTTGAAGGCTT	2203
QY	2013	GGCACTCGGATATCTTGGCCCCCAGACCTCT	TACCCCTTCCCTGACACGAGCTGGTATT	2072
DB	2204	GGCACTCGGATATCTTGGCCCCCAGACCTCT	TACCCCTTCCCTGACACGAGCTGGTATT	2263
QY	2073	TGCGCACAGAGTCTCTACATTTCTATCTTGCT	CTCAGCCATCTACGAGGACAGTCCCAAGTT	2132
DB	2264	TGCGCACAGAGTCTCTACATTTCTATCTTGCT	CTCAGCCATCTACGAGGACAGTCCCAAGTT	2323
QY	2133	ACTCTGCCCTCAGAGCTGACAGCCAGCTGCC	ACACTTTGGGAGACCAAGTCTATTCTGTGCGCA	2192
DB	2324	ACTCTGCCCTCAGAGCTGACAGCCAGCTGCC	ACACTTTGGGAGACCAAGTCTATTCTGTGCGCA	2383
QY	2193	GGCGGACAGACCCAAAGTGA	CAGAGCTGACTTCGCGCGGAGCTGGCATGAAGAGAGCCCTT	2252
DB	2384	GGCGGACAGACCCAAAGTGA	CAGAGCTGACTTCGCGCGGAGCTGGCATGAAGAGAGCCCTT	2443
QY	2253	TTGAAAGACAGTTTAAACGCAGAGAGCTGCC	AAATGGAAATTCGAGAGAGCATCATGTTCAG	2312
DB	2444	TTGAAAGACAGTTTAAACGCAGAGAGCTGCC	AAATGGAAATTCGAGAGAGCATCATGTTCAG	2503
QY	2313	AGAACAGGTCACGGGAAGAGCTGGGAAAGT	GGGCAGTGGGCAGTGGCATGAAGAGAGCCCTT	2372
DB	2504	AGAACAGGTCACGGGAAGAGCTGGGAAAGT	GGGCAGTGGGCAGTGGCATGAAGAGAGCCCTT	2563
QY	2373	TGGAATATCATTTGAGGTCCTCGTAGAAGAA	AGACACTTGTGACTTCTATAGACAATTTTTT	2432
DB	2564	TGGAATATCATTTGAGGTCCTCGTAGAAGAA	AGACACTTGTGACTTCTATAGACAATTTTTT	2623
QY	2433	TTTCTTGTTCCAAAAAAATTC	CCCTCTAAATCTGAAATATATATATATATAT	2492
DB	2624	TTTCTTGTTCCAAAAAAATTC	CCCTCTAAATCTGAAATATATATATATATAT	2683
QY	2493	ATTTTGTGAAAAATCGAGCTATG	TGTATAAAGCAACAGGTGGTCAACCCAGTGT	2552
DB	2684	ATTTTGTGAAAAATCGAGCTATG	TGTATAAAGCAACAGGTGGTCAACCCAGTGT	2743
QY	2553	TCTTAAACATCTGCATTTGAGAGATCAGCT	AAATCTCTCTCAACAAAAATCGAAGGCGAG	2612
DB	2744	TCTTAAACATCTGCATTTGAGAGATCAGCT	AAATCTCTCTCAACAAAAATCGAAGGCGAG	2803
QY	2613	ATGTAGAAATCCCCCTTAGACGAGGAA	AAACCAATTTATTCAGTGAATATACATCTCTCT	2672
DB	2804	ATGTAGAAATCCCCCTTAGACGAGGAA	AAACCAATTTATTCAGTGAATATACATCTCTCT	2863
QY	2673	TGTTCTTTAAAAAACCAAGTGTCTTTGGTGT	TGGAGACAAAAATCCCTPACCAATTTTCCAC	2732
DB	2864	TGTTCTTTAAAAAACCAAGTGTCTTTGGTGT	TGGAGACAAAAATCCCTPACCAATTTTCCAC	2922
QY	2733	GTTGTGCTACTAAGAGATCTCAAAATAT	TAGTCTTTTTCGCGAACCTTCCATPAGTACCTT	2792
DB	2923	GTTGTGCTACTAAGAGATCTCAAAATAT	TAGTCTTTTTCGCGAACCTTCCATPAGTACCTT	2982
QY	2793	TAGCGCTCAGACTCAGCCAGCTTGGGGGT	CAGGTAGGTAGACCTGTWAGGACAGAGCC	2852
DB	2983	TAGCGCTCAGACTCAGCCAGCTTGGGGGT	CAGGTAGGTAGACCTGTWAGGACAGAGCC	3042
QY	2853	TAGTGGTAAATCCAAAGAGAAATGATCCT	ATCCAAAGCTGATTCACAAACCCACCGCTCACC	2912
DB	3043	TAGTGGTAAATCCAAAGAGAAATGATCCT	ATCCAAAGCTGATTCACAAACCCACCGCTCACC	3102
QY	2913	TGACAGCCGAGGACAGAGCATCTCTGCTGG	ACCGACATTAGGGGCTTCCCAAGG	2972
DB	3103	TGACAGCCGAGGACAGAGCATCTCTGCTGG	ACCGACATTAGGGGCTTCCCAAGG	3162
QY	2973	TCTACCTTTAGACAAACCCAGTACCTC	AGACAGGAAAGTCGGGGCTTTGACCACTACCAT	3032
DB	3163	TCTACCTTTAGACAAACCCAGTACCTC	AGACAGGAAAGTCGGGGCTTTGACCACTACCAT	3222

RESULT 6

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US-10-108-260A-2429
; Sequence 2429, Application US/10108260A
; Publication No. US2004000560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US2004000560a1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2429
; LENGTH: 1916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2429

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Query Match 53.9%; Score 1795.4; DB 15; Length 1916;
Best Local Similarity 95.5%; Pred. No. 0;

QY	1328	CTCAAGCTGTGCACTCGAGAGCAAAATGAACCTGTCCCTGTGTTCTCAGAGGTGGA	1387
Db	1	CTCAAGCTGTGCACTCGAGAGCAAAATGAACCTGTCCCTGTGTTCTCAGAGGTGGA	60
QY	1388	CAGAAAGCGAGAGCGCCCTCAGTCCACCTGTGCGCACTGTGCTACCTCAGAGCGACGA	1447
Db	61	CAGAAAGCGAGAGCGCCCTCAGTCCACCTGTGCGCACTGTGCTACCTCAGAGCGACGA	120
QY	1448	GGACAAAGGCGCGTGCATCCGCCAGCGTCCACGCGTCCGAGCGTCAGCCCGTCG	1507
Db	121	GGACAAAGGCGCGTGCATC-----	139
QY	1508	TTAGAGGACAGCCCGCTGTGTACAGGCGTCACTGGGCTGCACCTGTCGCGACAGCGCTG	1567
Db	140	-----CGCAGACAGCGCTG	153
QY	1568	GAAGCAGCAATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAAATCAGTTTCATATTC	1627
Db	154	GAAGCAGCAATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAAATCAGTTTCATATTC	213
QY	1628	GCCAGATGCGAGCATCCTTACATGCGTTCCTTCATCAGAGATGCTTTGGATATCTAC	1687
Db	214	GCCAGATGCGAGCATCCTTACATGCGTTCCTTCATCAGAGATGCTTTGGATATCTAC	273
QY	1688	AAACCTTCCACTCTCTGGATGGGACCAACAGCTATGCGAGTTCTCCCTGTTCAGGAA	1747
Db	274	AAACCTTCCACTCTCTGGATGGGACCAACAGCTATGCGAGTTCTCCCTGTTCAGGAA	333
QY	1748	CTATCGGAGCAGACTCCCGAAACAGTCTCTGTATAGGAGGAAGCCAGCATCCCCAAG	1807

334 CTATCGGAGGAGCTCCGGAACAGTCTCTGATAGGAGGAGCCAGCATCCCCAGAAG 393
1808 CTGCGAGACCGGAGGCTTTAGACAGCGAGAGGAGATTCGATTCGGTTCAGAACGAGC 1867
394 CTGCGAGACCGGAGGCTTTAGACAGCGAGAGGAGATTCGATTCGGTTCAGAACGAGC 453
1868 AGCAGTGGCAGCGCCAGAGGTCCTTTTATCTCCACTGCTGATCGAAGTGGGAGCGTGGAG 1927
454 AGCAGTGGCAGCGCCAGAGGTCCTTTTATCTCCACTGCTGATCGAAGTGGGAGCGTGGAG 513
1928 GACAAATTACCAACAGAGTCTCTTTTGGGCTTTTCCACCGAGCAGCAGCCTCAGGAAG 1987
514 GACAAATTACCAACAGAGTCTCTTTTGGGCTTTTCCACCGAGCAGCAGCCTCAGGAAG 573
1988 TGTGCTGGCTGGGCTTTAAGGCTGGCACTCGATATCTTGGCCGCCAGAGCTTACC 2047
574 TGTGCTGGCTGGGCTTTAAGGCTGGCACTCGATATCTTGGCCGCCAGAGCTTACC 633
2048 CTTCCCTGATCAGCAGAGTGGTATTTTGGCCACAGAGTCTCACAATTTCTACTCTGCTCA 2107
634 CTTCCCTGATCAGCAGAGTGGTATTTTGGCCACAGAGTCTCACAATTTCTACTCTGCTCA 693
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694 GCCATCTAGGAGGAGTGCAGTTACTCTGCTTACAGCTGAGCAGCTGCCCACTTGC 753
2168 GGAGACCAAGTCTATTCTGTGCGAGCGGCGAGAGCCAAAGTGACAGCTGACTCGCGG 2227
754 GGAGACCAAGTCTATTCTGTGCGAGCGGCGAGAGCCAAAGTGACAGCTGACTCGCGG 813
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814 CGAGCTGGCTGAAGAGAGCGCCCTTTGAAAGCAGTTTAAACGAGAGCTGCCAAATG 873
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994 TTGTCAGTCTTATAGACAATTTTCTTCTGTCACAAAATAATCCCTGTAATCTGA 1053
2468 AATATATATGTACATACATATATTTTGGAAATGAGCTATGCTGTAAGAACAC 2527
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2588 TCTCTCAACAAAATGGAAGGCGAGATGCTAGATCCCTCAGCGAGGAGAACCAT 2647
1174 TCTCTCAACAAAATGGAAGGCGAGATGCTAGATCCCTCAGCGAGGAGAACCAT 1233
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1234 TTATTCAGTGAATTACATCTCTTGTCTTAAAAAGCAAGTGTCTTTGGTGTGGAG 1293
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1294 GACAAAATCCCTACCATTTTCCAGGTTGCTACTAAGATCTCAATATTAGTCTTT 1352
2768 GTCCGGACCTTCCATAGTACACCTTAGCGCTGAGCTGAGCCAGCTTGGGGTCAAGTA 2827
1353 GTCCGGACCTTCCATAGTACACCTTAGCGCTGAGCTGAGCCAGCTTGGGGTCAAGTA 1412
2828 GGTAGACCTGTGAGGAGCAGAGCTTAGTGAATCCAAAGAGAAATGATCTTATCCAA 2887
1413 GGTAGACCTGTGAGGAGCAGAGCTTAGTGAATCCAAAGAGAAATGATCTTATCCAA 1472

2888 GCTGATTCAAAACCCACGCTCACCTGACAGCGGAGGACACGAGGATCACTCTGCTGGA 2947
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1533 CGGACCAATTAGGGGCTTTGCCAGGCTTACCTTAGAGCAAAACCCAGTACCTCAGACAGGA 1592
3008 AAGTCGGGCTTTGACCACTACCAATCTCTGATGCCAATTTCTAGGCATTTGTAATAGG 3067
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3068 TAGTCTAGCTAGTACACCTTTTTCAGACCAATTTCAAACTGTCTATGCACAAAATTTCCGCTGG 3127
1653 TAGTCTAGCTAGTACACCTTTTTCAGACCAATTTCAAACTGTCTATGCACAAAATTTCCGCTGG 1712
3128 GCCTAGATGGAGATAATTTTTTTTCTCTCAGCTTTATGAAGAGAGGAAACTCTCTTA 3187
1713 GCCTAGATGGAGATAA-TTTTTTTTCTCTCAGCTTTATGAAGAGAGGAAACTCTCTTA 1771
3188 GGATTCAGCTGAACCCAGGAACTGGCAACATCAGGATTTAAGCTAAGGTTGGGAGGC 3247
1772 GGATTCAGCTGAACCCAGGAACTGGCAACATCAGGATTTAAGCTAAGGTTGGGAGGC 1831
3248 TAACGAGTCTACCTCCCTCTTTTGAATCAAGAAATTTTAAAAATGGGATTTGTAATCC 3307
1832 TAACGAGTCTACCTCCCTCTTTTGAATCAAGAAATTTTAAAAATGGGATTTGTAATCC 1891
3308 TTTAAATAAAGATGAATCTGTTTC 3332
1892 TTTAAATAAAGATGAATCTGTTTC 1916

RESULT 7

US-10-094-749-673
; Sequence 673, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 673
; LENGTH: 2102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-673

11021	TGTCCTTGGCTGTCTCAGAGGGTGGACAGAAAACGAGACGGCCCTCAGTCACCCCTGTGC	1080
11022	CGATCTGTCTACCTCAGAGCGCAGCAGGACAAAGGCGCGGTGATCCCGCAGCGTGCCCGAG	1482
11023	CGATCTGTCTACCTCAGAGCGCAGCAGGACAAAGGCGCGGTGATCCCGCAGCGTGCCCGAG	1140
11024	CGTCCAGCGTGCACCGCGTGTGTAGAGACAGCCGCTGGTACAGGGCGCTCAGTGG	1200
11025	GCTGCACCTGTCGCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTCT	1602
11026	GCTGCACCTGTCGCGCAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTCT	1260
11027	GGATATCAAAATCAGTTTCATATTACAGCCAGCATGCGCAGATCTTTACATGCGTTCCTCT	1662
11028	GGATATCAAAATCAGTTTCATATTACAGCCAGCATGCGCAGATCTTTACATGCGTTCCTCT	1320
11029	ATCAGAAAGATGCTTTGGAACTACTACAAACCTTCCACTACTCTGGATGGGACCAACAAGCT	1722
11030	ATCAGAAAGATGCTTTGGAACTACTACAAACCTTCCACTACTCTGGATGGGACCAACAAGCT	1380
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11032	ATGCCAGTTCTCCCTGTTTCAGAACTATCGGAGCAGACTCCCGAAACCACTCTCTGATAA	1840
11033	GGAGGAGCCAGCATCCCCAAGAAGCTGCAGACCCGAGGCGCTTCAGACAGCCAGAGACAA	1842
11034	GGAGGAGCCAGCATCCCCAAGAAGCTGCAGACCCGAGGCGCTTCAGACAGCCAGAGACAA	1500
11035	GCATTTGCAATTCGGTTCAGAACACGACGAGTGGCACCGCCAGAGGTCCTTTTATCTCC	1902
11036	GCATTTGCAATTCGGTTCAGAACACGACGAGTGGCACCGCCAGAGGTCCTTTTATCTCC	1560
11037	ACTGCATCGAAGTGGAGCGTGGAGGACAAATTTACACACACAGCTTCCTTTTCGCGCTTC	1962
11038	ACTGCATCGAAGTGGAGCGTGGAGGACAAATTTACACACACAGCTTCCTTTTCGCGCTTC	1620
11039	CACCAGCCAGCAGCACTCACGAAGTCTGCTGGCCCTGGGCGCTTAAGGCGTGGCACTCGGA	2022
11040	CACCAGCCAGCAGCACTCACGAAGTCTGCTGGCCCTGGGCGCTTAAGGCGTGGCACTCGGA	1680
11041	TATCTTGGCCCCCAGACCTCTACCCCTTCCTGCACGACGCTGGTATTTTGCACAGA	2082
11042	TATCTTGGCCCCCAGACCTCTACCCCTTCCTGCACGACGCTGGTATTTTGCACAGA	1740
11043	GTCCCTCACACTTCTACTCTGCTCAGCCATCTACGAGGACGACGAGTACTCTCGCTA	2142
11044	GTCCCTCACACTTCTACTCTGCTCAGCCATCTACGAGGACGACGAGTACTCTCGCTA	1800
11045	CAGCTGCAGCCAGCTGCCCACTTGGGAGACCAAGTCTATTCTGTGCGCAGCGCGCAGAA	2202
11046	CAGCTGCAGCCAGCTGCCCACTTGGGAGACCAAGTCTATTCTGTGCGCAGCGCGCAGAA	1860
11047	CCCAAGTGCACGAGCTGACTCGCGCGGAGCTGGCATGAAGAGGCCCTTTTGAAGAACA	2262
11048	CCCAAGTGCACGAGCTGACTCGCGCGGAGCTGGCATGAAGAGGCCCTTTTGAAGAACA	1920
11049	GTTTTAAACGCAAGCTGCCCCAATGGAAATTTGGAGAGAGCATCATGTCCAGAGAACAGGTC	2322
11050	GTTTTAAACGCAAGCTGCCCCAATGGAAATTTGGAGAGAGCATCATGTCCAGAGAACAGGTC	1980
11051	ACGGGAAGAGCTGGGAAAGTGGCGAGTCACTTTCGGGCGAGCATGGAAATCAT	2382
11052	ACGGGAAGAGCTGGGAAAGTGGCGAGTCACTTTCGGGCGAGCATGGAAATCAT	2040
11053	TGAGGCTCTCTGAGAGAAAGACACTTGTGACTTCTATAGACAAATTTTTTTTCTTGTTC	2442
11054	TGAGGCTCTCTGAGAGAAAGACACTTGTGACTTCTATAGACAAATTTTTTTTCTTGTTC	2100
11055	AC 2444	

Db 2101 AC 2102

RESULT 8

US-10-072-012-255
Sequence 255, Application US/10072012
Publication No. US2004003493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Ji
APPLICANT: Gangolli, Beha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier, Jr., Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Riegez, Daniel K.
APPLICANT: Burgess, Catherine E.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-258

CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,517

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,412

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/266,406

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/267,057

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

PRIOR FILING DATE: 2001-02-08

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 255

LENGTH: 2200

TYPE: DNA

ORGANISM: Homo sapiens

US-10-072-012-255

Query Match 52.3%; Score 1742; DB 12; Length 2200;

Best Local Similarity 90.5%; Pred. No. 0;

Matches 1991; Conservative 0; Mismatches 0; Indels 209; Gaps 4;

502 ACCATTACATCATCGTGGGCAAAATTAAGAGAGAGGTGGGAAAGAGAGCTTATTGTTGTC 561

1 ACCATTACATCATCGTGGGCAAAATTAAGAGAGAGGTGGGAAAGAGAGCTTATTGTTGTC 60

562 ATGCCCATGAGATGATTGGAACCTCAATTTGTTACTGAGAGGTTGGTGGCTCTGCTGAA 621

Db 61 ATGCCCATGAGATGATTGGAACCTCAATTTGTTACTGAGAGGTTGGTGGCTCTGCTGAA 120
Qy 622 AGTGGAAACGAAAAAGTGTCTTAATTGATAGCGGCCCATTTGTGAAATACAAATACATCC 681
Db 121 AGTGGAAACGAAAAAGTGTCTTAATTGATAGCGGCCCATTTGTGAAATACAAATACATCC 180
Qy 682 CACATTTTGGAAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGCAACAG 741
Db 181 CACATTTTGGAAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAGCGAAGTTGCAACAG 240
Qy 742 GACAAAGTGTTAATTACAGAGCTCATCCAGCACTTCCAGCGAACATA-----AG 789
Db 241 GACAAAGTGTTAATTACAGAGCTCATCCAGCACTTCCAGCGAACATAAAGGTAAACCGCTCAG 300
Qy 790 GTTGACATTAATTGACAGTCAGAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATTTGCC 849
Db 301 GTTGACATTAATTGACAGTCAGAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATTTGCC 360
Qy 850 TCTCTCTCTTACAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAGAGCTTCAAC 909
Db 361 TCTCTCTCTTACAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAGAGCTTCAAC 420
Qy 910 TCTGTTCACTGCTTGC----- 926
Db 421 TCTGTTCACTGCTTGCAGGTTTATCTTAGTGGGTTTGTGAGTTCTCTCGTTGTTTC 480
Qy 927 ----- 926
Db 481 CTTGGCTCTGTGAAGGAAATCCACTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTA 540
Qy 927 ----- 926
Db 541 CTTGTTGCCAACATTTGGGCCAACCCGAATCTTCCAAATCTTATCTTGGCTGCCAGCA 600
Qy 927 -----AGAGCTGATGACAGAGAAATGGGATGGTATGTGTTAAATGCCAGC 973
Db 601 GATGTCTCTCAACAAGGAGCTGATGACAGAGAAATGGGATGGTATGTGTTAAATGCCAGC 660
Qy 974 ATACCTGTCCAAAGCCGTGACTTTATCCCGAGTCTCATTTCCCTGCGTGGCTGTGAAT 1033
Db 661 ATACCTGTCCAAAGCCGTGACTTTATCCCGAGTCTCATTTCCCTGCGTGGCTGTGAAT 720
Qy 1034 GACAGCTTTTGTGAGAAAAATTTTGGCGTGGTGGGACAAATCAGTAGATTTTCATT----- 1087
Db 721 GACAGCTTTTGTGAGAAAAATTTTGGCGTGGTGGGACAAATCAGTAGATTTTCATTGGTAA 780
Qy 1088 -----GAGAAAGCAAAAGCCCTCAATGGATGTGTTCTAGTGCATGTTAGCT 1135
Db 781 TTGACTTATACAGAGAAAGCAAAAGCCCTCAATGGATGTGTTCTAGTGCATGTTAGCT 840
Qy 1136 GGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGATGGACATGCT 1195
Db 841 GGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGATGGACATGCT 900
Qy 1196 TTAGATGAAGCTTAC---AGATTTGTGAAAGAAAAAGACCTACTATATCTCCAACTTC 1252
Db 901 TTAGATGAAGCTTACAGGAGATTTGTGAAAGAAAAAGACCTACTATATCTCCAACTTC 960
Qy 1253 AATTTTCTGGGCCAACTCTCGGACTATGAGAGAGATTTAAGAACCCAGACTGGAGCATCA 1312
Db 961 AATTTTCTGGGCCAACTCTCGGACTATGAGAGAGATTTAAGAACCCAGACTGGAGCATCA 1020
Qy 1313 GGGCCAAAGAGCAAACTCAAGCTGTGCACTCCCTGGAGAGAGCAAAATGAACCTGTCCCTGCT 1372
Db 1021 GGGCCAAAGAGCAAACTCAAGCTGTGCACTCCCTGGAGAGAGCAAAATGAACCTGTCCCTGCT 1080
Qy 1373 GTCTCAGAGGTGGACAGAAAGCCAGAGCGCCCTCAGTCCACCTGTGCCGACTGCT 1432
Db 1081 GTCTCAGAGGTGGACAGAAAGCCAGAGCGCCCTCAGTCCACCTGTGCCGACTGCT 1140
Qy 1433 ACCTCAGAGCGCAGGAGCAAAAGCGCCCTGATCCGCGAGCGTGCAGCGGCGGCCAGCGTCCAGC 1492

Db 121 AGTGAACGGAAGAGTGTCTAATTGATAGCGGCCATTGTGGAATACAAATACATCC 180
Qy 682 CACATTTTGGAGAGCCATTAATTAATCAACTGCTCCAGCTTATGAAGCGAAGTTCCAAACAG 741
Db 181 CACATTTTGGAGAGCCATTAATTAATCAACTGCTCCAGCTTATGAAGCGAAGTTCCAAACAG 240
Qy 742 GACAAAGTGTAAATACAGAGTCTATCCAGCAATTCAGCGAAACATAGAGTTGACATTGAT 801
Db 241 GACAAAGTGTAAATACAGAGTCTATCCAGCAATTCAGCGAAACATAGAGTTGACATTGAT 300
Qy 802 TGCAGTCAAGAGTTGATTTACGATCAAGCTCCAAAGAGTTGAGCTCTCTCTCTCA 861
Db 301 TGCAGTCAAGAGTTGATTTACGATCAAGCTCCAAAGAGTTGAGCTCTCTCTCTCA 360
Qy 862 GACTGTTTTCTCACTGTACTCTCGGTAACTGGAGAGAGCTTCACTCTGTTCACTG 921
Db 361 GACTGTTTTCTCACTGTACTCTCGGTAACTGGAGAGAGCTTCACTCTGTTCACTG 420
Qy 922 CTTGC----- 926
Db 421 CTTGCAGGTGGTTTGTCTGAGTTCTCTGTTGTTTCCCTGGCCCTCTGTGAAGGAATATCC 480
Qy 927 ----- 926
Db 481 ACTTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTTGCCAAATTTGGGCCAACC 540
Qy 927 -----AGAGCTGATG 937
Db 541 CGAATCTTCCCAATCTTATCTTGGCTGCCAGCAGATGCTCTCAACAGAGCTGATG 600
Qy 938 CAGCAGATGGGATTTGTTATGTTTAAATGCGAGCAATACCTGTCCAAAGCCTGACTTT 997
Db 601 CAGCAGATGGGATTTGTTATGTTTAAATGCGAGCAATACCTGTCCAAAGCCTGACTTT 660
Qy 998 ATCCCGAGTCTCAATTTCTCGTGTGCTGTGATGACAGCTTTTGTGAGAAATTTTG 1057
Db 661 ATCCCGAGTCTCAATTTCTCGTGTGCTGTGATGACAGCTTTTGTGAGAAATTTTG 720
Qy 1058 CCGTGGTTGGACAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGGATGTGT 1117
Db 721 CCGTGGTTGGACAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGGATGTGT 780
Qy 1118 CTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATG 1177
Db 781 CTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATG 840
Qy 1178 AAGAGATGGACATGCTTTTAGATCAAGCTTACAGATTTGTGAAGAAAGAAAGACCTACT 1237
Db 841 AAGAGATGGACATGCTTTTAGATCAAGCTTACAGATTTGTGAAGAAAGAAAGACCTACT 900
Qy 1238 ATATCTCMAACTTCAATTTTCTGGGCCAACTCTCTGGAATAAGAGAGATTAAGAAC 1297
Db 901 ATATCTCMAACTTCAATTTTCTGGGCCAACTCTCTGGAATAAGAGAGATTAAGAAC 960
Qy 1298 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTTGGAGAGCCAAAT 1357
Db 961 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTTGGAGAGCCAAAT 1020
Qy 1358 GAACCTGTCCTCTGCTCTCAGAGGTTGGACAGAAAGCAGAGACGCCCTCAGTCCACCC 1417
Db 1021 GAACCTGTCCTCTGCTCTCAGAGGTTGGACAGAAAGCAGAGACGCCCTCAGTCCACCC 1080
Qy 1418 TGTGCGACTCTGCTACCTCAGAGCAGCAGGACAAAGCCCGTGCATCCCGCAGCGTG 1477
Db 1081 TGTGCGACTCTGCTACCTCAGAGCAGCAGGACAAAGCCCGTGCATCCCG----- 1132
Qy 1478 CCGAGCTGCCAGGCTGAGCGCTGCTGTTAGAGGACAGCCCGCTGCTACAGCGCTC 1537
Db 1133 -CCAGCTACCCAGCGTGACGCGTGTGTTAGAGGACACCCCGCTGCTACAGCGCTC 1191
Qy 1538 AGTGGGCTGCACCTGTCCGAGACAGGCTGGAGACAGCAATAGCTCAAGCGTTCTTC 1597
Db 1192 AGTGGGCTGCACCTGTCCGAGACAGGCTGGAGACAGCAATAGCTCAAGCGTTCTTC 1251

Qy 1598 TCTCTGGATATCAAAATCAAGTTTCAATTTACCCAGCATGGCAGCATCTTACATGGCTTC 1657
Db 1252 TCTCTGGATATCAAAATCAAGTTTCAATTTACCCAGCATGGCAGCATCTTACATGGCTTC 1311
Qy 1658 TCTCTCATCAGAAAGATGCTTTGGAAATCTACAAACCTTCCACTACTCTGGATGGACCAAC 1717
Db 1312 TCTCTCATCAGAAAGATGCTTTGGAAATCTACAAACCTTCCACTACTCTGGATGGACCAAC 1371
Qy 1718 AAGTATGCCAGTTCTCCCTGTTTCAGAACTATCGGAGCAGACTCCCGAAACAGTCTCT 1777
Db 1372 AAGTATGCCAGTTCTCCCTGTTTCAGAACTATCGGAGCAGACTCCCGAAACAGTCTCT 1431
Qy 1778 GATAAGGAGGAGCCAGCATCCCAAGAGCTGCAGACCCCGAGGCTTCCAGACAGCCAG 1837
Db 1432 GATAAGGAGGAGCCAGCATCCCAAGAGCTGCAGACCCCGAGGCTTCCAGACAGCCAG 1491
Qy 1838 AGCAAGCGATTTCATTTCCGTTCAGAACCCAGCAGCTGCGCACCGCCAGAGGTCCCTTTTA 1897
Db 1492 AGCAAGCGATTTCATTTCCGTTCAGAACCCAGCAGCTGCGCACCGCCAGAGGTCCCTTTTA 1551
Qy 1898 TCTCCACTGCAATCGAAGTGGAGCGTGGAGACAATTTACACACCAGCTTCCCTTTTGGC 1957
Db 1552 TCTCCACTGCAATCGAAGTGGAGCGTGGAGACAATTTACACACCAGCTTCCCTTTTGGC 1611
Qy 1958 CTTTCCACCCAGCAGCAGCACTCAGAAAGTCTGCTGGCCCTTAAAGGGCTGGCAC 2017
Db 1612 CTTTCCACCCAGCAGCAGCACTCAGAAAGTCTGCTGGCCCTTAAAGGGCTGGCAC 1671
Qy 2018 TCGGATATCTTGGGCCCCAGACCTCTACCCCTTCCCTGACCCAGCAGCTGTTTGGC 2077
Db 1672 TCGGATATCTTGGGCCCCAGACCTCTACCCCTTCCCTGACCCAGCAGCTGTTTGGC 1731
Qy 2078 ACAGAGTCTCTCACACTTCTACTCTGCTCTGCTCAGCCATCTACGAGGAGCTGCGAGTACTCT 2137
Db 1732 ACAGAGTCTCTCACACTTCTACTCTGCTCTGCTCAGCCATCTACGAGGAGCTGCGAGTACTCT 1791
Qy 2138 GCCTACAGCTCAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGCGAGCGG 2197
Db 1792 GCCTACAGCTCAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGCGAGCGG 1851
Qy 2198 CAGAGCCCAAGTGCAGAGCTGACTCCGCGGAGCTGGCATGAAGAGAGCCCTTTGAA 2257
Db 1852 CAGAGCCCAAGTGCAGAGCTGACTCCGCGGAGCTGGCATGAAGAGAGCCCTTTGAA 1911
Qy 2258 AAGCAGTTTAAACCCAGAAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCCAGAAAC 2317
Db 1912 AAGCAGTTTAAACCCAGAAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTCCAGAAAC 1971
Qy 2318 AGGTCACGGGAGAGCTGGGAAAGTGGGAGAGTGGCATGTAGCTTTTGGGCGAGATGGAA 2377
Db 1972 AGGTCACGGGAGAGCTGGGAAAGTGGGAGAGTGGCATGTAGCTTTTGGGCGAGATGGAA 2031
Qy 2378 ATCATTTGAGGTCTCTCTGAGAAAGAGACACTTTGTGACTTC 2417
Db 2032 ATCATTTGAGGTCTCTCTGAGAAAGAGACACTTTGTGACTTC 2071

RESULT 10

US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494.3

Query Match      49.8%; Score 1660; DB 9; Length 1998;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1834; Conservative 0; Mismatches 0; Indels 164; Gaps 1;

QY 562 ATGCCCATGAGATGATGGAACCTCAAAATGTTACTGAGAGTGTGCTCTGTGAA 621
DB 1 ATGCCCATGAGATGATGGAACCTCAAAATGTTACTGAGAGTGTGCTCTGTGAA 60
QY 622 AGTGGACGGAAGAGCTGCTAAATGATAGCGGCCAATTTGTGAATACAAATACATCC 681
DB 61 AGTGGACGGAAGAGCTGCTAAATGATAGCGGCCAATTTGTGAATACAAATACATCC 120
QY 682 CACATTTTGAAGCCATTAATATCAATCACTGCCAAGCTTATGAAGCGAAGTTGCAACAG 741
DB 121 CACATTTTGAAGCCATTAATATCAATCACTGCCAAGCTTATGAAGCGAAGTTGCAACAG 180
QY 742 GACAAAGTGTAAATACAGAGCTATCCAGCATTCAGCGAAACATAGGTTGACATTGAT 801
DB 181 GACAAAGTGTAAATACAGAGCTATCCAGCATTCAGCGAAACATAGGTTGACATTGAT 240
QY 802 TGCAGTCAGAAAGTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCTTCA 861
DB 241 TGCAGTCAGAAAGTGTAGTTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCTTCA 300
QY 862 GACTGTTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921
DB 301 GACTGTTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 922 CTTCG----- 926
DB 361 CTTCGAGTGGTGTGCTGAGTCTCTCTGTTGTTTCCCTGGGCTCTGTGAAGGAAATCC 420
QY 927 ----- 926
DB 421 ACTCTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACTGTTGCCAACTTGGGCCAAC 480
QY 927 -----AGAGGCTGATG 937
DB 481 CGAATCTTCCCAATCTTTATCTTGGCTGCAGGAGATGTCCTCAAGAGGCTGATG 540
QY 938 CAGCAGAAATGGGATGGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGGCTGACTTT 997
DB 541 CAGCAGAAATGGGATGGTTATGTTTAAATGCCAGCAATACCTGTCCAAAGGCTGACTTT 600
QY 998 ATCCCGAGTCTCAATTTCTGCGTGCCTGTGAATGACAGCTTTTGTGAGAAATTTTG 1057
DB 601 ATCCCGAGTCTCAATTTCTGCGTGCCTGTGAATGACAGCTTTTGTGAGAAATTTTG 660
QY 1058 CCGTGGTTGGCAAAATCAGTAGATTTTCAATGGAGAAAGCAAAAGCCCTCCATGGATGTT 1117
DB 661 CCGTGGTTGGCAAAATCAGTAGATTTTCAATGGAGAAAGCAAAAGCCCTCCATGGATGTT 720
QY 1118 CTAGTGCACTGTTTGTAGTGGGATCTCCGCTCCGCCACCATTCGCTATCGCTACATCATG 1177
DB 721 CTAGTGCACTGTTTGTAGTGGGATCTCCGCTCCGCCACCATTCGCTATCGCTACATCATG 780
QY 1178 AAGAGGATGGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAGACCTACT 1237
DB 781 AAGAGGATGGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAGACCTACT 840
QY 1238 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAGGAGATTAAGAAC 1297
DB 841 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAGGAGATTAAGAAC 900
QY 1298 CAGACTGAGCATCAGGGCCAAAGAGCAAACTCAGCTGCTGACCTGGAGAGCCAAAT 1357
DB 901 CAGACTGAGCATCAGGGCCAAAGAGCAAACTCAGCTGCTGACCTGGAGAGCCAAAT 960
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RESULT 11
US-10-377-072-27
Sequence 27, Application US/10377072
Publication No. US2004009501A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Miyoung
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MP103-0180WNLN
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)....(1998)
US-10-377-072-27

Query Match 49.8%; Score 1660; DB 15; Length 1998;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1834; Conservative 0; Mismatches 0; Indels 164; Gaps 1;
QY 562 ATGGCCCATGATGATGGAGTCAAAATGTTACTGAGAGGTTGGTGGCTCTGCTGGAA 621
DB 1 ATGGCCCATGATGATGGAGTCAAAATGTTACTGAGAGGTTGGTGGCTCTGCTGGAA 60
QY 622 AGTGAACGGAAGAAAGTCTGCTAAATGATAGCGCGCCATTGTGGAAATACATATACATCC 681
DB 61 AGTGAACGGAAGAAAGTCTGCTAAATGATAGCGCGCCATTGTGGAAATACATATACATCC 120
QY 682 CACATTTGGAAGCCATTAATATCACTGCTCCAGCTTATGAGCGAGGTTGCAACAG 741
DB 121 CACATTTGGAAGCCATTAATATCACTGCTCCAGCTTATGAGCGAGGTTGCAACAG 180
QY 742 GACAAAGTGAATATACAGAGCTCATCCAGCATTCACGAGAAATAGAGTTGACATTGAT 801
DB 181 GACAAAGTGAATATACAGAGCTCATCCAGCATTCACGAGAAATAGAGTTGACATTGAT 240

QY 802 TGCAGTCAGAAAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCCTCTCTCTTCA 861
DB 241 TGCAGTCAGAAAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCCTCTCTCTTCA 300
QY 862 GACTGTTTCTCACTGACTGTTCTGGTAAATCTGGAGAGAGCTTCAACTCTGTTCACCTG 921
DB 301 GACTGTTTCTCACTGACTGTTCTGGTAAATCTGGAGAGAGCTTCAACTCTGTTCACCTG 360
QY 922 CTTCG----- 926
DB 361 CTTGAGGTGGGTTTGTCTGAGTTCTCTCGTTGTTTCCCTGGCCCTCTGTGAGAGAAATCC 420
QY 927 ----- 926
DB 421 ACTCTAGTCCCTACCTGCAATTTCTCAGCCCTTGTCTTACCTGTTGCCAACAATGGGCCCAACC 480
QY 927 -----AGGAGCTGATG 937
DB 481 CGAATTCCTCCCAATCTTATCTTGGCTGCCGCGAGATGTCCTCAACAGGAGCTGATG 540
QY 938 CAGCAGAAATGGGATTGGTTATGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 597
DB 541 CAGCAGAAATGGGATTGGTTATGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 600
QY 998 ATCCCGAGTCTCAATTCCTGGTGTGCTGTGAATGACAGCTTTTGTGAGAAAAATTTG 1057
DB 601 ATCCCGAGTCTCAATTCCTGGTGTGCTGTGAATGACAGCTTTTGTGAGAAAAATTTG 660
QY 1058 CCGTGTGGGACAAATCAGTAGATTTTCAATGAGAAAGCAAAAGCCTCCCAATGGATGTT 1117
DB 661 CCGTGTGGGACAAATCAGTAGATTTTCAATGAGAAAGCAAAAGCCTCCCAATGGATGTT 720
QY 1118 CTAGTGCACTGTTTGTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATG 1177
DB 721 CTAGTGCACTGTTTGTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATG 780
QY 1178 AAGAGGATGGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACT 1237
DB 781 AAGAGGATGGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACT 840
QY 1238 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTCGCACTATGAGAAAGAGATTAAAGAC 1297
DB 841 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTCGCACTATGAGAAAGAGATTAAAGAC 900
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DB 901 CAGACTGGAGATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGGAGAGCCAAAT 960
QY 1358 GAACCTGTCCCTGCTGCTCAGAGGGTGGACAGAAAGCGAGACGCCCTCAGTCCACCC 1417
DB 961 GAACCTGTCCCTGCTGCTCAGAGGGTGGACAGAAAGCGAGACGCCCTCAGTCCACCC 1020
QY 1418 TGTGCCGACTCTGTACTCTCAGAGGAGGAGCAAAAGCCCGTGCATCCCGCCAGCGTG 1477
DB 1021 TGTGCCGACTCTGTACTCTCAGAGGAGGAGCAAAAGCCCGTGCATCCCGCCAGCGTG 1080
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DB 1081 CCAGCGTGTCCGCGTGTGAGCGTGTGAGAGGAGCAGCCCGTGTGAGAGGCTC 1140
QY 1538 AGTGGGTGCACTGTCTCCGAGACAGGCTGGAGAGCAGCAATAAGCTCAAGGGTCTCTTC 1597
DB 1141 AGTGGGTGCACTGTCTCCGAGACAGGCTGGAGAGCAGCAATAAGCTCAAGGGTCTCTTC 1200
QY 1598 TCTCTGATATCAATCAGTTTTCATATTAGCGAGGATGGAGCATCTTACATGGCTTC 1657
DB 1201 TCTCTGATATCAATCAGTTTTCATATTAGCGAGGATGGAGCATCTTACATGGCTTC 1260
QY 1658 TCTCTCAGAGATGCTTTGGAAATCTACAACCTTCCACTACTCTGATGGAGCCAC 1717
DB 1261 TCTCTCAGAGATGCTTTGGAAATCTACAACCTTCCACTACTCTGATGGAGCCAC 1320
QY 1718 AAGTATGCCAGTTTCTCCCTGTTCAGGAACTATGAGAGCAGACTCCCGAAACCAAGTCT 1777

;; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
;; FILE REFERENCE: 7388-73435
;; CURRENT APPLICATION NUMBER: US/10/220,891
;; CURRENT FILING DATE: 2003-03-07
;; PRIOR APPLICATION NUMBER: JP 2000/140387
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: JP 2000/159195
;; PRIOR FILING DATE: 2000-03-07
;; NUMBER OF SEQ ID NOS: 108
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 85
;; LENGTH: 787
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (2)..(2)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (4)..(5)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (7)..(7)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (12)..(13)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (16)..(19)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (23)..(23)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (31)..(31)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (574)..(574)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (635)..(635)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (660)..(660)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (725)..(725)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (750)..(750)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (752)..(752)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (755)..(755)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (760)..(760)

;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (763)..(763)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (765)..(765)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (771)..(771)
;; OTHER INFORMATION: a, t, c, g, unknown or other
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: (777)..(777)
;; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-220-891-85

Query Match 17.9%; Score 595; DB 15; Length 787;
Best Local Similarity 96.6%; Pred. No. 4.6e-175;
Matches 659; Conservative 0; Mismatches 18; Indels 5; Gaps 5;

QY 2651 TTCAGTGAATTACACATCCTCTTCTTCTTAAAGCAAGTGTCTTTGGTGGAGGAC 2710
DB 45 TACTGGGAATTACACATCCTCTTCTTCTTAAAGCAAGTGTCTTTGGTGGAGGAC 104
QY 2711 AAATCCCTTACCAATTTTCCACGTTGTCTTACTAAGAGATCTCAATATATTAGTCTTTGTC 2770
DB 105 AAATCCCTTACCAATTTT-CACGTTGTCTTACTAAGAGATCTCAATATATTAGTCTTTGTC 163
QY 2771 CGGACCTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTAGGT 2830
DB 164 CGGACCTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTAGGT 223
QY 2831 AGACCTCTTAGGGACAGAGCGCTAGTGTGTAATCCAAAGAAATGATCTTATCAAGCT 2890
DB 224 AGACCTCTTAGGGACAGAGCGCTAGTGTGTAATCCAAAGAAATGATCTTATCAAGCT 283
QY 2891 GATTCAAAACCCAGCTCACCCTGACAGCGGAGGACACGAGCATCACTCTGTGGACGG 2950
DB 284 GATTCAAAACCCAGCTCACCCTGACAGCGGAGGACACGAGCATCACTCTGTGGACGG 343
QY 2951 ACCATTAGGGCCCTTGCCAGGCTACCTTTAGAGCAAAACCCAGTACCTCAGACGAGAAAG 3010
DB 344 ACCATTAGGGCCCTTGCCAGGCTACCTTTAGAGCAAAACCCAGTACCTCAGACGAGAAAG 403
QY 3011 TCGGGCTTGACCACTACCATATCTGTAGCCCATTTCTAGGCATTTGTAATAGTAG 3070
DB 404 TC-GGGCTTTGACCACTACCATATCTGTAGCCCATTTCTAGGCATTTGTAATAGTAG 462
QY 3071 GTAGCTAGTCACACTTTTTCAGACCAATTCAAACTGTCTATGCAAAATTCCTGTGGGCC 3130
DB 463 GTAGCTAGTCACACTTTTTCAGACCAATTCAAACTGTCTATGCAAAATTCCTGTGGGCC 521
QY 3131 TAGATGGAGATAATTTTTTTTCTCTCAGCTTTATGAAGAGGGAAGAACTGTCTAGGA 3190
DB 522 TAGATGGAGATAA-TTTTTTTTCTCTCAGCTTTATGAAGAGGGAAGAACTGTCTAGGA 580
QY 3191 TTCAGCTCAACCCAGGAACTCGGCAACATCAAGATTTAAGCTTAAGTTGGGAGGCTAA 3250
DB 581 TTCAGCTCAACCCAGGAACTCGGCAACATCAAGATTTAAGCTTAAGTTGGGAGGCTAA 640
QY 3251 CGAGTCTACCTCCCTCTTTTGAATCAAGAAATGTTTAAATGGGATTTGTCATCTCTTT 3310
DB 641 CGAGTCTACT-CCCTCTTGAATCAAGAAATGTTTAAATGGGATTTGTCATCTCTTT 699
QY 3311 AAATAAGATGAACCTTGGTTTC 3332
DB 700 AAATAAGATGAACCTTGGTTTC 721

RESULT 14

US-09-764-853-158
; Sequence 158, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 158
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-158

Query Match 16.1%; Score 537.4; DB 9; Length 877;
Best Local Similarity 98.5%; Pred. No. 6e-157; Indels 6; Gaps 3;
Matches 574; Conservative 0; Mismatches 6; Indels 6; Gaps 3;
QY 285 GTGGAATGGTTATTCAGTCATCTCTTTATGAATCAAAATGTGAGGGGCTGCTTTGTGAC 344
Db 15 GTGGAATGGTTATTCAGTCATCTCTTTATGAATCAAAATGTGAGGGGCTGCTTTGTGAC 74
QY 345 GGAGTCCTTTGCAAGAGCATCAACGGGAAAGAGAAAGAGACATTCACCTTGGAGGGCTC 404
Db 75 GGAGT-CTTTGCAAGAGCATCAACGGGAAAGAGAAAGAGACATTCACCTTGGAGGGCTC 133
QY 405 TTCTGAAATGGTTTAACTCTCTCTTTTGGCAGTCACACAGCCTGACCTCATACACT 464
Db 134 TTCTGAAATGGTTTAACTCTCTCTTTTGGCAGTCACACAGCCTGACCTCATACACT 193
QY 465 TTTAGTACATGGAGTGGCTTGAGCTTTGAGCAGACACACCCATTACATCATCTGTCGCAAT 524
Db 194 TTTAGTACATGGAGTGGCTTGAGCTTTGAGCAGACACACCCATTACATCATCTGTCGCAAT 253
QY 525 TAAAGAGAGAGTGGGAAAGAGGACTTATTGTTGTCAGTCCCATGAGATGATTGGAAC 584
Db 254 TAAAGAGAGAGTGGGAAAGAGGACTTATTGTTGTCAGTCCCATGAGATGATTGGAAC 313
QY 585 TCAATTTGTACTGAGAGTGTGTGCTCTGCTGGAAGTGAACGGAAAGTGTCTGCT 644
Db 314 TCAATTTGTACTGAGAGTGTGTGCTCTGCTGGAAGTGAACGGAAAGTGTCTGCT 373
QY 645 AATTGATAGCCGCCATTTGGAATACAAATACATCCACATTTTGGAGCCATTAAAT 704
Db 374 AATTGATAGCCGCCATTTGGAATACAAATACATCCACATTTTGGAGCCATTAAAT 433
QY 705 CAATGCTCCAGCTTATGAAGCAAGGTGCAACAGGCAAAAGTGTAAATTACAGACT 764
Db 434 CAATGCTCCAGCTTATGAAGCGAA-GTTGCAACAGGCAAAAGTGTAAATTACAGACT 492
QY 765 CATCCAGACTTCAGCAACATAGGTTGACATTTGATTCAGTCAGAGGTTGATGTTTA 824
Db 493 CATCCAGACTTCAGCAACATAGGTTGACATTTGATTCGA-TCAGAGGTTGATGTTTA 551
QY 825 CGATCAAGCTCCCAAGATGTTGCTCTCTCTCTCTCAGACTGT 867
Db 552 CGATCAAGCTCCCAAGATGTTGCTCTCTCTCTCTCAGACTGT 594

RESULT 15

US-09-918-995-25801
; Sequence 25801, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25801
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(478)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-25801

Query Match 12.3%; Score 409.2; DB 10; Length 478;
Best Local Similarity 98.6%; Pred. No. 6.4e-117; Indels 2; Gaps 2;
Matches 433; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 2499 GGAATAATGAGCTATGTTGTAAGCAACAGGTGGATCAACCCAGTTGTACTCTCTTAA 2558
Db 42 GGAATAATGAGCTATGTTGTAAGCAACAGGTGGATCAACCCAGTTGTACTCTCTTAA 101
QY 2559 CATCTGCATTTGAGAGATCAGCTAATCTTCTCAACAAAAATGGAAGGAGATGCTA 2618
Db 102 CATCTGCATTTGAGAGATCAGCTAATCTTCTCAACAAAAATGGAAGGAGATGCTA 161
QY 2619 GAATCCCCCTAGCGAGGAGAAACCAATTTTATTCAGTGAATTACACATCTCTTGTCT 2678
Db 162 GAATCCCCCTAGCGAGGAGAAACCAATTTTATTCAGTGAATTACACATCTCTTGTCT 221
QY 2679 TAAAAAAGCAAGTGTCTTTTGGTGTGGAGGACAAAAATCCCTACCATTTT-CACGTTGTG 2738
Db 222 TAAAAAAGCAAGTGTCTTTTGGTGTGGAGGACAAAAATCCCTACCATTTT-CACGTTGTG 280
QY 2739 CTACTAAGAGATCTCAAAATATTAGTCTTTGTCGGACCTTCCATAGTACACCTTAGCGC 2798
Db 281 CTACTAAGAGATCTCAAAATATTAGTCTTTGTCGGACCTTCCATAGTACACCTTAGCGC 340
QY 2799 TGAGACTGAGCCAGCTTGGGGGTGAGGTAGGTAGAGCCCTGTTAGGGACAGAGCCTAGTG 2858
Db 341 TGAGACTGAGCCAGCTTGGGGGTGAGGTAGGTAGAGCCCTGTTAGGGACAGAGCCTAGTG 400
QY 2859 TAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCAAAACCCAGCTCAGCTGACAG 2918
Db 401 -AAATCCAGAGAAATGATCTTATCCAAAGCTGATTCAAAACCCAGCTCAGCTGACAG 459
QY 2919 CCGAGGACACAGCATCA 2937
Db 460 NCGAGGACACAGCATCA 478

Search completed: February 28, 2004, 01:16:00
Job time: 1085 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2004, 18:43:34 ; Search time 8123 Seconds
(without alignments)
12249.266 Million cell updates/sec

Title: US-09-964-277-20
Perfect score: 3332
Sequence: 1 gagagaagagaagataata.....ataaagatgaactgtgttc 3332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	896.4	26.9	1201	13	BX332176
2	858	25.8	1060	12	BM546940
3	834.6	25.0	883	13	BQ945892
4	827.8	24.8	881	13	BQ930140

5	809.8	24.3	913	13	BUL70187
6	809.6	24.3	859	13	BQ933499
7	786.2	23.6	974	13	BQ951695
8	777	23.3	798	13	EX110818
9	766.4	23.0	903	12	BG482429
10	741.2	22.2	891	13	BQ670989
11	736.4	22.1	1148	12	BM906608
12	717.8	21.5	740	10	AW963248
13	688.4	20.7	720	14	CA944683
14	641.2	19.2	920	10	BE897795
15	632	18.5	663	13	EX479029
16	615.4	18.5	660	12	BI917706
17	607.4	18.2	3325	11	AK035652
18	606.6	18.2	983	12	BG155198
19	603.2	18.1	752	13	BQ432082
20	574.4	17.2	650	9	AU253268
21	574	17.2	593	12	BM930580
22	551.8	16.6	685	14	CB165612
23	551.4	16.5	557	9	AI807619
24	541.2	16.2	621	9	AV703072
25	539	16.2	539	9	AI659120
26	537	16.1	548	9	AI637845
27	537	16.1	554	9	AW014773
28	536.8	16.1	693	9	AV701628
29	534.8	16.1	543	9	AI936544
30	534.8	16.1	790	12	BI661614
31	533	16.0	551	9	AI674392
32	511	15.3	723	13	BU708175
33	508.8	15.3	524	10	BF432802
34	493	14.8	496	9	AI678804
35	492	14.8	862	13	BQ770036
36	490.8	14.7	743	14	CF727802
37	485	14.6	796	10	BF983182
38	484.6	14.5	514	12	BM684128
39	483.4	14.5	524	10	BF758523
40	482	14.5	511	12	BM930518
41	479.4	14.4	739	28	AZ850285
42	466.6	14.0	546	10	BE232856
43	465	14.0	898	13	BQ721265
44	462.4	13.9	631	28	BH039241
45	462.4	13.9	1067	10	BF135687

ALIGNMENTS

RESULT 1
BX332176
LOCUS
DEFINITION
BX332176 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC008YN23 5-PRIME, mRNA sequence.
ACCESSION
BX332176
VERSION
BX332176.1 GI:30335119
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1201)
Li W.B., Gruber C., Jeasee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6659.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC008CG12QP1&cluster=6659.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

1201 bp mRNA linear EST 02-MAY-2003
BX332176 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC008YN23 5-PRIME, mRNA sequence.
ACCESSION
BX332176
VERSION
BX332176.1 GI:30335119
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1201)
Li W.B., Gruber C., Jeasee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6659.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC008CG12QP1&cluster=6659.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Faraday Avenue Genoscope sequence ID : CS0DC008CG12QPi.

FEATURES

Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC008YN23"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 26.9%; Score 896.4; DB 13; Length 1201;
Best Local Similarity 97.9%; Pred. No. 7e-232;
Matches 920; Conservative 7; Mismatches 11; Indels 2; Gaps 2;

QY 2391 CCTGAGAGAGACACTTGTGACTCTCTATACAGCAATTTTCTTCTGTTCACAAAAA 2450
DB 60 CCGGGATAGAGACACTTGTGACTCTCTATACAGCAATTTTCTTCTGTTCACAAAAA 119
QY 2451 ATTCCCTGTAATCTGAATATATATATGATACATATATATTTTGGAAATGGAGC 2510
DB 120 ATTCCCTGTAATCTGAATATATATATGATACATATATATTTTGGAAATGGAGC 179
QY 2511 TATGGTGTAAAGACAGGTGATCAACCCAGTTGTTACTCTCTTAACATCTGCATTG 2570
DB 180 TATGGTGTAAAGACAGGTGATCAACCCAGTTGTTACTCTCTTAACATCTGCATTG 239
QY 2571 AGAGATCAGTAAATCTCTCTCAACAAAAATGGAAGGCGAGATCTAGAAATCCCCCTA 2630
DB 240 AGAGATCAGTAAATCTCTCTCAACAAAAATGGAAGGCGAGATCTAGAAATCCCCCTA 299
QY 2631 GACGGAGGAAACCAATTTATTCAGTGAATACATCTCTTGTCTTAAAAAGCAAG 2690
DB 300 GACGGAGGAAACCAATTTATTCAGTGAATACATCTCTTGTCTTAAAAAGCAAG 359
QY 2691 TGTCTTTGGTGTGGAGGACAAATCCCTACATTTTCCAGCTGTGCTACTAAGAGAT 2750
DB 360 TGTCTTTGGTGTGGAGGACAAATCCCTACATTTTCCAGCTGTGCTACTAAGAGAT 418
QY 2751 CTCAATATTAGTCTTTGTCCGAGCCCTTCCATAGTACACCTTAGCGTGTAGACTGAGCC 2810
DB 419 CTCAATATTAGTCTTTGTCCGAGCCCTTCCATAGTACACCTTAGCGTGTAGACTGAGCC 478
QY 2811 AGCTTGGGGTCAGGTAGGTAGACCTGTGTAGGACAGAGCTAGTGTGAATCCAGAG 2870
DB 479 AGCTTGGGGTCAGGTAGGTAGACCTGTGTAGGACAGAGCTAGTGTGAATCCAGAG 538
QY 2871 AAATGATCTTATCAAAAGCTGATTCAAAACCCAGCTCACCTGACAGCCGAGGACAG 2930
DB 539 AAATGATCTTATCAAAAGCTGATTCAAAACCCAGCTCACCTGACAGCCGAGGACAG 598
QY 2931 AGCATCACTCTGTGACAGGACATTAGGGGCTTGGCCAGGCTTACCTTAGAGCAACC 2990
DB 599 AGCATCACTCTGTGACAGGACATTAGGGGCTTGGCCAGGCTTACCTTAGAGCAACC 658
QY 2991 CAGTACTCTAGACAGGAAAGTGGGGCTTTGACCACTACCATATCTGCTAGCCCATTTTC 3050
DB 659 CAGTACTCTAGACAGGAAAGTGGGGCTTTGACCACTACCATATCTGCTAGCCCATTTTC 718
QY 3051 TAGGCATTTGGAATAGGTAGGTAGTGTACACATTTTTCAGACCAATTCAACTGTCTAT 3110
DB 719 TAGGCATTTGGAATAGGTAGGTAGTGTACACATTTTTCAGACCAATTCAACTGTCTAT 778
QY 3111 GCACAAAATTCGGCGCTAGATGGAGATAATTTTTTTTCTCTCAGCTTTTATGAAG 3170
DB 779 GCACAAAATTCGGCGCTAGATGGAGATAATTTTTTTTCTCTCAGCTTTTATGAAG 838
QY 3171 AGAAGGGAATCTGTCTAGGATTCAGCTGAACCAACAGGAACCTGGCAACATCACGATTTA 3230

DB 839 AGAAGGGAATCTGTCTAGGATTCAGTGAACCAACAGGAACCTGGCAACATCACGATTTA 898
QY 3231 AGCTAAGGTTGGAGGCTTAACGAGTCTACCTCCCTCTTTGTAATCAAGAATTTGTTAA 3290
DB 899 AGCTAAGGTTGGAGGCTTAACGAGTCTACCTCCCTCTTTGTAATCAAGAATTTGTTAA 958
QY 3291 AATGGGATTCATCTCTTAAATTAAGATGAATCTGTT 3330
DB 959 AATGGGATTCATCTCTTAAATTAAGATGAATCTGTT 997

RESULT 2
BM546940
LOCUS BM546940
DEFINITION AGENCOURT_6491295 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723711
5', mRNA sequence.
ACCESSION BM546940
VERSION BM546940.1 GI:18780310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12711 row: m column: 24
High quality sequence stop: 737.

FEATURES
Location/Qualifiers
1. .1060
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5723711"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary; pool of 3; Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

ORIGIN
Query Match 25.8%; Score 858; DB 12; Length 1060;
Best Local Similarity 94.7%; Pred. No. 1.8e-221;
Matches 933; Conservative 0; Mismatches 35; Indels 17; Gaps 4;

QY 927 AGGAGCTGATCCAGCAATGGATTTGTTATGTTAAATGCCAGCAATACCTGTCCAA 986
DB 49 AGGAGCTGATCCAGCAATGGATTTGTTATGTTAAATGCCAGCAATACCTGTCCAA 108
QY 987 AGCCTGACTTTATCCCGAGTCTCATTTTCTCGCTGTGCCTGTGAATGACAGCTTTTGTG 1046
DB 109 AGCCTGACTTTATCCCGAGTCTCATTTTCTCGCTGTGCCTGTGAATGACAGCTTTTGTG 168
QY 1047 AGAAAATTTTCCCGTGTGTGCAAAATCAGTAGATTTTCATTGAGAAAGCAAGCCTCCA 1106
DB 169 AGAAAATTTTCCCGTGTGTGCAAAATCAGTAGATTTTCATTGAGAAAGCAAGCCTCCA 228

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QY 1107 ATGGATGTCTTCTAGTGCACTGTTTAGTGGGAACTCCCGCTCCGCCACCATCGCTATCG 1166
Db 229 ATGGATGTCTTCTAGTGCACTGTTTAGTGGGAACTCCCGCTCCGCCACCATCGCTATCG 288
QY 1167 CTTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTGTGAAAGAAA 1226
Db 289 CTTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTGTGAAAGAAA 348
QY 1227 AAAGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTGGACTATGAGAGA 1286
Db 349 AAAGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTGGACTATGAGAGA 408
QY 1287 AGATTAAAGAACAGACTGGAGCATCAGGCCCCAAAGAGCAAACTCAAGCTGCTGCACCTGG 1346
Db 409 AGATTAAAGAACAGACTGGAGCATCAGGCCCCAAAGAGCAAACTCAAGCTGCTGCACCTGG 468
QY 1347 AGAAGCCAAATCAACTGTCTCCCTGCTGTCTCAGAGGTGGACAGAAAGCGAGAGCCCC 1406
Db 469 AGAAGCCAAATCAACTGTCTCCCTGCTGTCTCAGAGGTGGACAGAAAGCGAGAGCCCC 528
QY 1407 TCAGTCCACCCCTGTGCCACTCTGTACTCTCAGAGGCGAGGCAAAAGGCCGCTGCATC 1466
Db 529 TCAGTCCACCCCTGTGCCACTCTGTACTCTCAGAGGCGAGGCAAAAGGCCGCTGCATC 588
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Db 589 CGC-----CCAGCGTACCCAGCGTGCAGCGTGCCTGTTAGAGGACAGCCCGCTGG 639
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QY 1826 TCAGACAGCCAGCAAGCG-----ATTGCATTGCTCAGAACCCAGCAGCTGCGAAC 1879
Db 939 TCAGACAGCCAGCAAGCGGATGTCATTGNTCAGAACCCAGCAGCTGCGAACCGCG 998
QY 1880 GCCAGAGGTCCTTTTATCTCCAC 1904
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RESULT 3
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LOCUS
DEFINITION BQ945892 883 bp mRNA linear EST 21-AUG-2002
AGENCY AGENCOURT 8926314 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6463045
5', mRNA sequence.
ACCESSION BQ945892
VERSION BQ945892.1 GI:22361370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 883)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
```

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2653 row: o column: 14
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/clone_lib="NIH_MGC_101"

/note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 25.0%; Score 834.6; DB 13; Length 883;
Best Local Similarity 98.5%; Pred. No. 3.9e-215;
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QY 1491 CGCTGACCGCTGCTGTTAGAGGACAGCCGCTGTGACAGGCGCTCAGTGGCTGCACC 1550
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5', mRNA sequence.
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VERSION BQ930140.1 GI:22345171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 881)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2648 row: h column: 21
High quality sequence stop: 676.
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/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/notes="Organ: lung; Vector: pOTF7; Site:1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 24.8%; Score 827.8; DB 13; Length 881;
Best Local Similarity 99.4%; Pred. No. 2.8e-213;
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DEFINITION AGENCOURT_7940023 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6007510
5', mRNA sequence.
ACCESSION BUI70187
VERSION BUI70187.1 GI:22684171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 913)
```

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
 Tissue Procurement: DCTD/BTP/Gaardar
 CNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

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FEATURES

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Query Match 24.3%; Score 809.8; DB 13; Length 913;
 Best Local Similarity 96.9%; Pred. No. 2.2e-208;
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BQ933499

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 5', mRNA sequence.

ACCESSION

BQ933499

VERSION

BQ933499.1 GI:22348892

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 859)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC

CNA Library Preparation: Rubin Laboratory
 CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

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FEATURES

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 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACAG(G) Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 24.3%; Score 809.6; DB 13; Length 859;
 Best Local Similarity 96.5%; Pred. No. 2.5e-208;
 Matches 827; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

QY 1191 TGCTTTTAGTGAAGCTTACAGATTGTGAAAGAAAAAGACCTACTATCTCTCAAACT 1250

Db 1 TGTCTTATAGTGAAGCTTACAGATTGTGGAAGAAAAAGACCTACTATATCTCCAACT 60
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QY 1791 CCAGCATCCCCAG 1850
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QY 1851 ATTCCGCTCAG 1910
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QY 1911 GAAGTGGAG 1970
Db 721 GAAGTGGAG 780
QY 1971 AGCAGACCTCAG 2028
Db 781 AGCAGACCTCAG 840

RESULT 7
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DEFINITION 5', mRNA sequence.
ACCESSION BO951695
VERSION BO951695.1 GI:22367173
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS NIH-MGC <http://mgi.nhl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-1@mail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM2650 row: f column: 05
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ORIGIN
Query Match 23.6%; Score 786.2; DB 13; Length 974;
Best Local Similarity 94.5%; Pred. No. 6.1e-202;
Matches 882; Conservative 0; Mismatches 38; Indels 13; Gaps 6;
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Db 541 TCTCCCGACAGAGGAG 600
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Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM2650 row: f column: 05
High quality sequence stop: 617.
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/note="Organ: lung; Vector: pOTB7; Site: 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."


```
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1431 row: m column: 23
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            /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
            Site_2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by
            Ling Hong in the laboratory of Gerald M. Rubin (University
            of California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 23.0%; Score 766.4; DB 12; Length 903;
Best Local Similarity 94.8%; Pred. No. 1.4e-196;
Matches 838; Conservative 0; Mismatches 36; Indels 10; Gaps 4;

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QY 927 AGGAGCTGATGCGAGCAATGGGATGGTATGTTAAATCCAGCAATACCTGTCCAA 986
DB 19 AGGAGCTGATGCGAGCAATGGGATGGTATGTTAAATCCAGCAATACCTGTCCAA 78
QY 987 AGCTGACTTTATCCCGAGTCTCATTTCTGCTGCTGCTGATGACAGCTTTTGTG 1046
DB 79 AGCTGACTTTATCCCGAGTCTCATTTCTGCTGCTGCTGATGACAGCTTTTGTG 138
QY 1047 AGAAATTTTCCGCTGGTGGCAATACAGTATTTCAATTCAGAAAGCAAAAGCTCCA 1106
DB 139 AGAAATTTTCCGCTGGTGGCAATACAGTATTTCAATTCAGAAAGCAAAAGCTCCA 198
QY 1107 ATGATGTGTTCTAGTGCATGTTAGCTGGGATCTCCGCTCCGCCACCATCGTATCG 1166
DB 199 ATGATGTGTTCTAGTGCATGTTAGCTGGGATCTCCGCTCCGCCACCATCGTATCG 258
QY 1167 CCTACATCATGAAGAGATGGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAA 1226
DB 259 CCTACATCATGAAGAGATGGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAA 318
QY 1227 AAGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGA 1286
DB 319 AAGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGA 378
QY 1287 AGATTGAACACAGATGGAGCATCAGGCGCAAGAGCAATCAAGTGTCTGCACCTGG 1346
DB 379 AGATTGAACACAGATGGAGCATCAGGCGCAAGAGCAATCAAGTGTCTGCACCTGG 438
QY 1347 AGAAGCCAAATGAACCTGTCCCTGCTGTTCTCAGAGGTGGAAGAAAGCGAGAGCGCCC 1406
DB 439 AGAAGCCAAATGAACCTGTCCCTGCTGTTCTCAGAGGTGGAAGAAAGCGAGAGCGCCC 498
QY 1407 TCAGTCCACCTGTGTCGCACTTGTCTACCTCAGAGGCGAGGCAAAAGGCCGTGCATC 1466
DB 499 TCAGTCCACCTGTGTCGCACTTGTCTACCTCAGAGGCGAGGCAAAAGGCCGTGCATC 558
QY 1467 CGCGCAGCGTGCAGCGCTGCGCCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGC 1526
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QY 1646 TT---ACATGGCTTCTCTCATCAGAAG-ATGCTTTGGAATACATAAACCTTCCACTAC 1701
DB 739 CITACATTGGCTTCATCTCTCATCAGAAGATGCTTTGGAATACATAAACCTTCCACTT 798
QY 1702 TCTGATGGGACCAACAAGC-----TATGCGAGTCTCCCTCTGTTCCAGAACTATCGAG 1756
DB 799 ACTCTGGATTGGGACCAACAAGGTTATGCCAGTTCTCCCTGTTCCAGAACTATCGAA 858
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5', mRNA sequence.
BQ670989
BQ670989.1 GI:21781823
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Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2374 row: f column: 06
High quality sequence stop: 633.
FEATURES
 source

ORIGIN

synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match 22.2%; Score 741.2; DB 13; Length 891;
Best Local Similarity 99.4%; Pred. No. 1e-189;
Matches 765; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1766 GAACACGCTCTGTAAAGAGGAGCAGCAGTCCCAAGAGCTGCAGAGCGCAGCCT 1825
Db 1 GAACACGCTCTGTAAAGAGGAGCAGCAGTCCCAAGAGCTGCAGAGCGCAGCCT 60

QY 1826 TCAGACAGCCAGCAGCAGTTCGCTCAGAACCCAGCAGCAGTGCACCGCCAG 1885
Db 61 TCAGACAGCCAGCAGCAGTTCGCTCAGAACCCAGCAGCAGTGCACCGCCAG 120

QY 1886 AGGTCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGACAATTACCAACAGC 1945
Db 121 AGGTCCCTTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGACAATTACCAACAGC 180

QY 1946 TTCCTTTTTCGGCTTTCACACAGCCAGCAGCAGTCCAGAGTCTGCTGGCCCTT 2005
Db 181 TTCCTTTTTCGGCTTTCACACAGCCAGCAGCAGTCCAGAGTCTGCTGGCCCTT 240

QY 2006 AAGGGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGC 2065
Db 241 AAGGGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGC 300

QY 2066 TGGTATTTTGCAGAGTCTCAGACTTCTACTCTGCTCAGCAGTCTCAGAGGAGT 2125
Db 301 TGGTATTTTGCAGAGTCTCAGACTTCTACTCTGCTCAGCAGTCTCAGAGGAGT 360

QY 2126 GCCAGTTACTTGCCTACAGCTGCAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCT 2185
Db 361 GCCAGTTACTTGCCTACAGCTGCAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCT 420

QY 2186 GTGCCAGCGGCGAGAGCCAGTGAAGAGCTGACTCGCGCGGAGCTGGCATGAAGAG 2245
Db 421 GTGCCAGCGGCGAGAGCCAGTGAAGAGCTGACTCGCGCGGAGCTGGCATGAAGAG 480

QY 2246 AGCCCTTTTGAAGACAGTCTTAAAGCGAGAGCTGCCAATGGAATTTGAGAGAGCATC 2305
Db 481 AGCCCTTTTGAAGACAGTCTTAAAGCGAGAGCTGCCAATGGAATTTGAGAGAGCATC 540

QY 2306 ATGTCAAGAGACAGTCAAGGAGAGCTGGGAAAGTGGGAGTCAAGTCAAGTCTTTG 2365
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QY 2366 GGCAGCATGGAATCATTTAGGTCTCCTGAGAGAGAGACACTTGTGACTTCTATAGCA 2425
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QY 2426 ATTTTCTTTTCTGTTCACAAAAAATTCCTGTAAATCTGAAATATATATATGTACATA 2485
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QY 2486 CATATATATTTT-GGAAATGGAGCTAT-GGTGTAAAGCAACAGGTGG 2533
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RESULT 11
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DEFINITION AGENCOURT_6621858 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5722534 5', mRNA sequence.
ACCESSION BM906608
VERSION BM906608.1 GI:19356987
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1148)
NIH-MGC <http://mhc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM12708 Row: 1 Column: 23
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/clone_lib="NIH_MGC_125"
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Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

FEATURES
source

ORIGIN

Query Match 22.1%; Score 736.4; DB 12; Length 1148;
Best Local Similarity 97.8%; Pred. No. 2.4e-188;
Matches 757; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 164 TCTCAGGCAATTGGAGCTCGCGGCCCAAGAGCTTTTCACTCCAGTGTAAAGCTGTGG 223
Db 3 TCTCAGGCAATTGGAGCTCGCGGCCCAAGAGCTTTTCACTCCAGTGTAAAGCTGTGG 62

QY 224 AGCCGGGAGCAAGGTAAAGAGATGATTAATCGCTGGCTGTCCAAAGCATCTTTGT 283
Db 63 AGCCGGGAGCAAGGTAAAGAGATGATTAATCGCTGGCTGTCCAAAGCATCTTTGT 122

QY 284 TGTGGAATGGTTATTCAGTCATCTTTATGATCAAAATGTGAGGGGTGCTTTGTGA 343
Db 123 TGTGGAATGGTTATTCAGTCATCTTTATGATCAAAATGTGAGGGGTGCTTTGTGA 182

QY 344 CGGAGTCTTTTGCAGAGCAGCATCAAGCGGAAAGAGAGACATTCATCTGGAGGGCT 403
Db 183 CGGAGTCTTTTGCAGAGCAGCATCAAGCGGAAAGAGAGACATTCATCTGGAGGGCT 242

QY 404 CTTCCTGAAATGGGTTTAACTCTCTTTTCCAGTCACACAGCCTGACCTCATACAC 463
Db 243 CTTCCTGAAATGGGTTTAACTCTCTCTTTTCCAGTCACACAGCCTGACCTCATACAC 302

QY 464 TTTTGTAGTCAATGGAGTGGCTGAGCCTTTGAGCACACACCATTAATCATCTGGCAAA 523
Db 303 TTTTGTAGTCAATGGAGTGGCTGAGCCTTTGAGCACACACCATTAATCATCTGGCAAA 362

QY 524 TTTAAGAGAGAGTGGGAAAGAGGACTTATTTGTTCTATGGCCCATGAGATGATGGAA 583
Db 363 TTTAAGAGAGAGTGGGAAAGAGGACTTATTTGTTCTATGGCCCATGAGATGATGGAA 422

QY 584 CTCAAAATTTTACTGAGAGTGTGCTCTCTGCTGAAAGTGGAAAGGAAAGTCTCTGC 643
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	TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368	
	TAG_LIB=UI-CF-FNO	
	TAG_SEQ=GGCTGTAGGC"	
ORIGIN		
	Query Match 20.7%; Score 688.4; DB 14; Length 720;	
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	Matches 700; Conservative 0; Mismatches 2; Indels 1; Gaps 1;	
QY	2630 AGACGAGAGAAACCAATTATTTCAGTGAATTACATCCCTCTGTGTTCTTAAAGACAA 2689	
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QY	2690 GTGTCTTTGGTGTGGAGACAAATCCCTACCAATTTCCACCTTGTGCTACTAAGAGA 2749	
DB	660 GTGTCTTTGGTGTGGAGACAAATCCCTACCAATTT-CACCTTGTGCTACTAAGAGA 602	
QY	2750 TCTCAAAATTAGTCTTTGTCGGACCTTCCATAGTACACCTTAGCGCTGAGACTGAGC 2809	
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QY	2810 CAGCTTTGGGGTTCAGGTAGTACCCCTGTTAGGGACAGACCTAGTGGTAAATCCAAGA 2869	
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QY	2990 CCAAGTACCTCAGACAGGAAGTCGGGGCTTTGACCACTACCATATCTGGTAGCCCAATTT 3049	
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Db 365 GCCCGTGCATCCCG-----CCAGCGTGCCAGCGTGCGCGTGTAGAGGA 415
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Db 476 CAATAGCTCAAGCGTTCCTCTCTCTGATATCAATCAGTTTCATATTCAGCCAGCAT 535
Qy 1636 GGCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAACTACTCAAACTTC 1695
Db 536 GGCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAACTACTCAAACTTC 595
Qy 1696 CACTACTCTGGATGGGACCAAGCATATGCCAGTTCCTCCCTGTTCAGGAACATCCGA 1755
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Db 655 GCAGACTCCCGAACCC---AGTGTGATAGGAGGAAGCCAGCATCCCAAGAGGTGCAGAC 711
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Db 712 CG-CAGGCTTCAGGAAGCCAGCAGCA 736

RESULT 15
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ACCESSION BX479029
VERSION BX479029.1 GI:31914415
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 663)
AUTHORS Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobz G., Han M. and Wiemann S.,
EST (Bahr A., Lauber J., Mewes H.W., Weil B., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
NO s1 sequence available.
This clone (DKFZp686J22208) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
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1. .663
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ORIGIN

Query Match 19.0%; Score 632; DB 13; Length 663;
Best Local Similarity 98.6%; Pred.No. 4.7e-160;
Matches 647; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

Qy 1062 GGTGGACAAATCAGTAGATTTCATT--GAGAAGCAAAGCCTCCATGATGATGTTCT 1119
Db 2 GGTGGACAAATCAGTAGATTTCANTTGACGAAAGCAAAGCCTCCATGATGATGTTCT 61
Qy 1120 AGTGCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAA 1179
Db 62 AGTGCACTGTTTGTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAA 121
Qy 1180 GAGGATGGACATGCTTTTGTAGATGAAGCTTACAGATTGTGAAAGAAAAGACCTACTAT 1239
Db 122 GAGGATGGACATGCTTTTGTAGATGAAGCTTACAGATTGTGAAAGAAAAGACCTACTAT 181
Qy 1240 ATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGACTATCAGAAGAGATTAAGAACCA 1299
Db 182 ATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGACTATCAGAAGAGATTAAGAACCA 241
Qy 1300 GACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTGCACTTGAAGAGATTAAGAACCA 1359
Db 242 GACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTGCACTTGAAGAGATTAAGAACCA 301
Qy 1360 ACTGTTCCTGTCTGTCTCAGAGGTGGACAGAAAGCGAGACGCCCTCAGTCCACCTGT 1419
Db 302 ACTGTTCCTGTCTGTCTCAGAGGTGGACAGAAAGCGAGACGCCCTCAGTCCACCTGT 361
Qy 1420 TGCCGACTCTGTCTACCTCAGAGGCGAGAGCAAAAGGCCCGTGCATCCGCCAGCGTGCC 1479
Db 362 TGCCGACTCTGTCTACCTCAGAGGCGAGAGCAAAAGGCCCGTGCATCCGCCAGCGTGCC 421
Qy 1480 CAGCGTGCCCGCGTGCAGCCGCTGCTTTAGAGGACAGCCCGCTGGTACAGGCGCTCAG 1539
Db 422 CAGCGTGCCCGCGTGCAGCCGCTGCTTTAGAGGACAGCCCGCTGGTACAGGCGCTCAG 481
Qy 1540 TGGGCTGCACCTGTCCGAGACAGCGCTGGAAGACAGCAATTAAGCTCAAGCGTTCCTTCTC 1599
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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(without alignments)

3706.310 Million cell updates/sec

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Perfect score: 517

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Ygapop 60.0 , Ygapext 60.0
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- 2: gb.htg:**
- 3: gb.in:**
- 4: gb.om:**
- 5: gb.ov:**
- 6: gb.pat:**
- 7: gb.ph:**
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- 9: gb.pr:**
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- 11: gb.sts:**
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- 21: em.or:**
- 22: em.ov:**
- 23: em.pat:**
- 24: em.ph:**
- 25: em.pl:**
- 26: em.ro:**
- 27: em.sts:**
- 28: em.un:**

RESULT 1

- 29: em.vi:**
- 30: em.htg.hum:**
- 31: em.htg.inv:**
- 32: em.htg.other:**
- 33: em.htg.mus:**
- 34: em.htg.pln:**
- 35: em.htg.rod:**
- 36: em.htg.nam:**
- 37: em.htg.vrt:**
- 38: em.sy:**
- 39: em.htgo.hum:**
- 40: em.htgo.mus:**
- 41: em.htgo.other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	517	100.0	1935	9	AY038927 Homo sapi
2	517	100.0	3332	6	AX441229 Sequence
3	488	94.4	1998	6	AX260342 Sequence
4	488	94.4	2102	6	AX713989 Sequence
5	488	94.4	2102	9	AK055973 Homo sapi
6	488	94.4	2732	6	AX130875 Sequence
7	488	94.4	3059	6	AX278461 Sequence
8	488	94.4	3104	6	AX405700 Sequence
9	488	94.4	3496	6	AX441210 Sequence
10	488	94.4	3521	9	AB052156 Homo sapi
11	488	94.4	3544	6	AX260340 Sequence
12	488	94.4	3566	9	AF506796 Homo sapi
13	488	94.4	3766	6	AX374994 Sequence
14	488	94.4	4790	6	BD171157 Novel gen
15	488	94.4	4790	6	BD183422 Novel gen
16	488	94.4	4790	9	AB051487 Homo sapi
17	472	91.3	5450	6	AX482439 Sequence
18	472	91.3	5450	6	AX482478 Sequence
19	455	88.0	2118	6	AX099933 Sequence
20	408	78.9	2200	6	AX921915 Sequence
21	394	76.2	172206	9	AC007619 Homo sapi
22	394	76.2	188344	2	AC131617 Homo sapi
23	387	74.9	2807	9	BC031643 Homo sapi
24	350	67.7	5111	6	AX482372 Sequence
25	304	58.8	2071	6	AX921917 Sequence
26	304	58.8	3284	9	BC042101 Homo sapi
27	178	34.4	1916	6	AX835305 Sequence
28	178	34.4	1916	9	AK098310 Homo sapi
29	66	12.8	242590	2	AC133722 Rattus no
30	66	12.8	244605	2	AC097818 Rattus no
31	66	12.8	250782	2	AC128093 Rattus no
32	63	12.2	2756	6	AX482444 Sequence
33	63	12.2	3861	10	AF345954 Mus muscu
34	63	12.2	4026	10	AF345953 Mus muscu
35	63	12.2	4827	10	AF345952 Mus muscu
36	63	12.2	4874	10	AB052157 Mus muscu
37	63	12.2	4943	10	BC059232 Mus muscu
38	63	12.2	4975	10	BC057321 Mus muscu
39	63	12.2	4992	10	AF345951 Mus muscu
40	61	11.8	201474	2	AC126692 Mus muscu
41	61	11.8	236589	2	AC118035 Mus muscu
42	50	9.7	301	6	AX524414 Sequence
43	50	9.7	301	6	AX553152 Sequence
44	45	8.7	749	6	AX868469 Sequence
45	45	8.7	749	6	BD148531 Primer fo

ALIGNMENTS

AY038927 1935 bp mRNA linear PRI 01-AUG-2001
LOCUS Homo sapiens truncated MAPK phosphatase 7 (MKP7) mRNA, complete
DEFINITION cds, alternatively spliced.
ACCESSION AY038927
VERSION AY038927.1 GI:15072488
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1935)
AUTHORS Montpetit, A., Boily, G. and Sinnett, D.
TITLE A detailed transcriptional map of the chromosome 12p12 tumor
suppressor locus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1935)
AUTHORS Montpetit, A., Boily, G. and Sinnett, D.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2001) Hemato-Oncology, Hopital Ste-Justine, 3175
Cote-Ste-Catherine, Montreal, QC H3T 1C5, Canada
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Best Local Similarity: 100.00% Mismatches: 0
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Db 368 GCTCAACTCTGTTCACTGCTGAGGAGCTGATGACAGAAATGGGATGGTTATG 427
QY 41 LeuAsnAlaSerAsnThrCysProLysProAspPheIleProGluSerHisPheLeuArg 60
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QY 101 SerArgSerAlaThrIleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAsp 120
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QY 221 SerLeuLeuGluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAsp 240
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QY 241 ArgLeuGluAspSerAsnLysLeuLysArgSerPheSerLeuAspLysSerValSer 260
Db 1028 AGCTGGAAGACAGCAATAAGCTCAAGCGTTCTCTCTGTGGATATCAATCAGTTTCA 1087
QY 261 TyrSerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGlu 280
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QY 281 TyrTyrLysProSerThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProVal 300
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QY 301 GlnGluLeuSerGluGlnThrProGluThrSerProAspLysGluGluAlaSerIlePro 320
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QY 341 ThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySer 360
Db 1328 ACCAGCAGCAGTGGCACCGCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGAGC 1387
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QY 421 AlaSerAlaIleTyrGlyLysAlaSerTyrSerAlaTyrSerCysSerGlnLeuPro 440
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QY 441 ThrCysGlyAspGlnValTyrSerValArgArgGlnLysProSerAspArgAlaAsp 460
Db 1628 ACTTGGAGAGCAAGTCTATTCTGTGGCAGGGGAGCAAGCAAGTGCAGAGCTGAC 1687
QY 461 SerArgArgSerTyrHisGluSerProPheGluLysGlnPheLysArgArgSerCys 480
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QY 501 ValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 517
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RESULT 2
AX441229 3332 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 20 from Patent WO0226997.
DEFINITION AX441229
ACCESSION AX441229
VERSION AX441229.1 GI:21665771
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Luche, R.M. and Wei, B.
Dsp-16 dual-specificity phosphatase
Patent: WO 0226997-A 20 04-APR-2002;
Ceptyr, Inc. (US)
FEATURES
source
1. 3332
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 3332
Score: 517.00 Matches: 517
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 21 AlaSerThrLeuPheThrCysLeuGlnGluLeuMetGlnAsnGlyIleGlyTrpVal 40
Db 902 GCTTCAACTCTGTTCACTGCTTGCAGAGCTGATGCAGCAGAATGGGATTGTTATGTG 961
QY 41 LeuAsnAlaSerAsnThrCysProLysProAspPheIleProGluSerHisPheLeuArg 60
Db 962 TTAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCTCGCT 1021
QY 61 ValProValAsnAspSerPheCysGluLysIleLeuProTrpLeuAspLysSerValAsp 80
Db 1022 GTGGCTGTGAATGACAGCTTTTGAGAAAATTTTGGCGTGGTTGGACAAATCAGTAGAT 1081
QY 81 PheIleGluLysAlaLysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIle 100
Db 1082 TTCATTGAGAAAGCAAAAGCCTCCAAATGATGTGTTCTAGTGACCTGTTTAGCTGGGATC 1141
QY 101 SerArgSerAlaThrIleAlaIleAlaTyrrIleMetLysArgMetAspMetSerLeuAsp 120
Db 1142 TCCCGCTCCGCACATCGCTATCGCTATCGCTATCATCATGAGAGGATGACATGCTTTAGAT 1201
QY 121 GluAlaTyrrArgPheValLysGluLysArgProThrIleSerProAsnPheAsnPheLeu 140
Db 1202 GAAGCTTACAGATTGTGAAAGAAAAAGACCTACTATATCTCCAAACTTCAATTTCTG 1261
QY 141 GlyGlnLeuLeuAspTyrrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLys 160
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RESULT 3

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Db 1862 ACCAGCAGCAGTGGCAGCCCGCCAGAGTCCCTTTTATCTCCATCGCATCAAGTGGGAGC 1921
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QY 381 ThrLysSerAlaGlyLeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThr 400
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Db 2222 TCGCGCGGAGCTGGCATGNAGAGACCCCTTTGAAACAGCTTTAAACGCGAGAGCTGC 2281
QY 481 GlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLys 500
Db 2282 CAAATGGAAATTTGGAGAGAGCATCATGTCCAGAGAACAGGTCCAGGAAAGAGCTGGGAAA 2341
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AX260342 AX260342 1998 bp DNA linear PAT 26-OCT-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0173059.
ACCESSION AX260342
VERSION AX260342.1 GI:16509305
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Meyers,R.A.
38692 and 21117: dual specificity phosphatase molecules and uses
therefor
Patent: WO 0173059-A 3 04-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
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Score: 488.00 Matches: 488
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Query Match: 94.39% Indels: 0
Gaps: 0
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RESULT 4
AX713989
LOCUS AX713989 2102 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 673 from Patent EP1293569.
ACCESSION AX713989
VERSION AX713989.1 GI:29888917
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,

Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuho, Y.

TITLE
JOURNAL
Full-length cDNAs
Patent: EP 1293569-A 673 19-MAR-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)

FEATURES
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/organism="Homo sapiens"
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ORIGIN


Alignment Scores:
Pred. No.: 0 Length: 2102
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 6 Gaps: 0

US-09-964-277-21 (1-517) x AX713989 (1-2102)

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QY 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
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QY 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
DB 887 AGACCTACTATATCTCCAAACTTCAATTTCTGGCCAACTCTCTGGCACTATGAGAAGAG 946
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DB 1787 AGTTACTCTGCTACAGCTGCAGCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTG 1846
QY 450 ArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
DB 1847 CGCAGGCGGCAAGACCAAGTCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGC 1906
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DB 1907 CCTTTTGAAGCAGTTTAAACGCAAGAGCTGCCAATGGAAATTTGGAGAGACATCATG 1966
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DB 1967 TCAGAGAACAGTCAAGGAGAGCTGGGAAAGTGGCAGTCACTAGCTTTCGGGC 2026
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AK055973
LOCUS
DEFINITION
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similar to DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48).
ACCESSION
AK055973
VERSION
AK055973.1 GI:16550835
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Masuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project

TITLE

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DEFINITION Sequence 2 from Patent WO0146394. 
ACCESSION AX180875
VERSION AX180875.1 GI:15132703
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Plowman,G.D., Martinez,R., Whyte,D., Manning,G., Sudarsanam,S.,
Hill,R.J. and Planagan,P.
TITLE Mammalian protein phosphatases
JOURNAL Patent: WO 0146394-A 2 28-JUN-2001;
Sugen, Inc. (US)
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AX278461

LOCUS AX278461 3059 bp DNA linear PAT 02-NOV-2001
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 ACCESSION AX278461
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 SOURCE Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini, Hominoidea; Homo.
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 Duecker, K.
 IDENTIFICATION OF A DUAL SPECIFICITY PHOSPHATASE: dusp-10
 TITLE Patent: WO 0177340-A 1 18-OCT-2001;
 JOURNAL MERCK PATENT GmbH (DE)
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 Score: 488.00 Matches: 488
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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DEFINITION Sequence 1 from Patent WO0173059.
ACCESSION AX260340
VERSION AX260340.1 GI:16509303
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Meyers, R.A.
TITLE 38692 and 21117: dual specificity phosphatase molecules and uses
therefor
JOURNAL Patent: WO 0173059-A 1 04-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
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ORIGIN
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Score: 488.00 Matches: 488
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QY 510 SerMetGluIleIleGluValSer 517
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RESULT 12
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LOCUS
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ACCESSION AF506796
VERSION AF506796.1 GI:25573087
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 3566)
AUTHORS Hoornaert, I., Marynen, P., Goris, J., Sciote, R. and Baens, M.
TITLE MAPK phosphatase DUSP16/MKP-7, a candidate tumor suppressor for chromosome region 12p12-13, reduces BCR-ABL-induced transformation
JOURNAL Oncogene 22 (49), 7728-7736 (2003)
PUBMED 14586399
REFERENCE 2 (bases 1 to 3566)
AUTHORS Hoornaert, I., Marynen, P. and Baens, M.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Department for Human Genetics-Flanders Interuniversity Institute for Biotechnology (VIB), Katholieke Universiteit Leuven, Herestraat 49, Leuven B-3000, Belgium
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ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 3566
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
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DEFINITION Sequence 17 from Patent WO210363.
ACCESSION AX374994
VERSION AX374994.1 GI:19169826
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tang, Y. T., Elliott, V. S., Ramkumar, J., Yao, M. G., Burford, N.,
Wang, Y. E., Stewart, E. A., Gandhi, A. R., Patterson, C., Lee, E. A.,
Hafalia, A. J., Lu, D. A., Tribouley, C. M., Griffin, J. A., Baughn, M. R.,
Yue, H., Warren, B. A., Nguyen, D. B. and Walla, N. K.
PROTEIN phosphatases
JOURNAL Patent: WO 0210363-A 17 07-FEB-2002;
Incyte Genomics, Inc. (US)
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Percent Similarity: 100.00% Conservative: 0
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Qy	410	TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla	429
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Ohara, C., Nagase, T. and Nakajima, D.		
TITLE	Novel gene and protein encoded thereby		
JOURNAL	Patent: WO 02052005-A 13 04-JUL-2002;		
SOURCE	KAZUSA DNA RESEARCH INSTITUTE, OSAMU OHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIMA		
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DEFINITION Novel genes and proteins encoded by the genes.
ACCESSION  BD183422
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 4750)
AUTHORS   Chara,O., Nagase,T. and Nakajima,D.
TITLE     Novel genes and proteins encoded by the genes
JOURNAL   Patent: JP 2002345492-A 135 03-DEC-2002;
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QY 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 2035 CCCTTTGAAAAGCAGTTTAAACGCAGAGCTGCCAAATGGATTTGGAGAGAGCATCATG 2094
QY 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2095 TCAGAGAACAGGTCAACGGGAGAGCTGGGAAAGTGGGAGTCAAGTCTAGCTTTTCGGGC 2154
QY 510 SerMetGluIleIleGluValSer 517
Db 2155 AGCATGGAAATCATTTGAGGTCTCC 2178
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Search completed: February 28, 2004, 03:08:22
Job time : 6077 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: February 28, 2004, 00:57:54 ; Search time 110 seconds
(without alignments)
2608.269 Million cell updates/sec

Title: US-09-964-277-21
Perfect score: 517
Sequence: 1 MLEPLSLQTVFLYFWNRR.....LGKVGQSFGSGMEIIIEVS 517

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Ygapop 60.0 , Ygapext 60.0
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues
Word size: 1

Total number of hits satisfying chosen parameters: 1360453

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Issued Patents NA -QWTF=fastcap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	94.4	1998	US-09-816-494-3	Sequence 3, Appli
2	488	94.4	2544	US-09-816-494-1	Sequence 1, Appli
3	20	3.9	2377	US-09-920-668-3	Sequence 3, Appli
4	12	2.3	2109	US-09-016-434-1135	Sequence 1135, App
5	12	2.3	2109	US-09-023-655-946	Sequence 946, App
6	9	1.7	320	US-09-389-681-310	Sequence 310, App
7	9	1.7	320	US-09-620-405B-310	Sequence 310, App
8	9	1.7	320	US-09-339-338-310	Sequence 310, App
9	9	1.7	320	US-09-433-826B-310	Sequence 310, App
10	9	1.7	320	US-09-604-287A-310	Sequence 310, App
11	9	1.7	320	US-09-834-759-310	Sequence 310, App
12	9	1.7	539	US-09-389-681-311	Sequence 311, App

C 13	9	1.7	539	4	US-09-620-405B-311	Sequence 311, App
C 14	9	1.7	539	4	US-09-339-338-311	Sequence 311, App
C 15	9	1.7	539	4	US-09-433-826B-311	Sequence 311, App
C 16	9	1.7	539	4	US-09-604-287A-311	Sequence 311, App
C 17	9	1.7	539	4	US-09-834-759-311	Sequence 311, App
C 18	9	1.7	944	4	US-09-371-671B-10	Sequence 10, Appl
19	9	1.7	1238	2	US-08-530-290-11	Sequence 11, Appl
20	9	1.7	1238	4	US-09-702-705-803	Sequence 803, App
21	9	1.7	1238	4	US-09-736-457-803	Sequence 803, App
22	9	1.7	1238	4	US-09-614-124B-803	Sequence 803, App
23	9	1.7	1238	4	US-09-671-325-803	Sequence 803, App
24	9	1.7	1238	4	US-09-589-184-803	Sequence 803, App
25	9	1.7	1619	4	US-09-702-705-801	Sequence 801, App
26	9	1.7	1619	4	US-09-736-457-801	Sequence 801, App
27	9	1.7	1619	4	US-09-614-124B-801	Sequence 801, App
28	9	1.7	1619	4	US-09-671-325-801	Sequence 801, App
29	9	1.7	1619	4	US-09-589-184-801	Sequence 801, App
30	9	1.7	1987	2	US-08-990-379-1	Sequence 1, Appli
31	9	1.7	1993	2	US-08-990-379-2	Sequence 2, Appli
32	9	1.7	2000	4	US-09-016-434-1291	Sequence 1291, App
33	9	1.7	2064	4	US-09-702-705-825	Sequence 825, App
34	9	1.7	2064	4	US-09-736-457-825	Sequence 825, App
35	9	1.7	2064	4	US-09-614-124B-825	Sequence 825, App
36	9	1.7	2064	4	US-09-671-325-825	Sequence 825, App
37	9	1.7	2064	4	US-09-589-184-825	Sequence 825, App
38	9	1.7	2109	4	US-09-702-705-826	Sequence 826, App
39	9	1.7	2109	4	US-09-736-457-826	Sequence 826, App
40	9	1.7	2109	4	US-09-614-124B-826	Sequence 826, App
41	9	1.7	2109	4	US-09-671-325-826	Sequence 826, App
42	9	1.7	2109	4	US-09-589-184-826	Sequence 826, App
43	9	1.7	2240	4	US-09-016-434-1100	Sequence 1100, App
44	9	1.7	4637	4	US-09-702-705-804	Sequence 804, App
45	9	1.7	4637	4	US-09-736-457-804	Sequence 804, App

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:
Pred. No.: 0 Length: 1998
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-816-494-3 (1-1998)

Qy	30	GlutMetGlnGlnAsnGlyVileGlyVtValLeuAsnAlaSerAsnThrCysProLys	49
Db	532	GAGTGTGTCAGCAGATGGATGGTGTATGCTTAATGCCAGCAATACCTGTCACAG	591
Qy	50	ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu	69

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Db 592 CTTGACCTTTATCCCGGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAG 651
Qy 70 LysIleLeuProThrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsn 89
Db 652 AAAATTTTGGCGTGTGGACAAATCAGTAGATTTTCATTGAGAAACAAAGCCCTCCAAAT 711
Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 712 GGAATGTTCTAGTGACCTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCC 771
Qy 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
Db 772 TACATCATGAAGAGGATGACATGCTTTTAGATGAAGCTTACAGATTGTGCAAGAAAAA 831
Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 832 AGACCTTACTATATCTCCAACTTCAATTTCTGGGCCCACTCTCGGACTATGGAAGAAG 891
Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
Db 892 ATTAAGACACAGACTGAGCATCAGGCCCAAGAGCAAACTCAAGCTGCTGCACCTGGAG 951
Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLeu 189
Db 952 AAGCCAAATGAACCTGCTGCTGCTCTCAGAGGGTGGACAGAAAGCGAGACGCCCTC 1011
Qy 190 SerProProCysAlaAspSerAlaThrSerGluAlaGlyGlnArgProValHisPro 209
Db 1012 AGTCACCTTGTCGCACTCTGCTACCTCAGAGGAGCAGACAGAAAGCCCGTGCATCCC 1071
Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1072 GCCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGT 1131
Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1132 CAGCGCTCAGTGGGTGCACTGCTCCGAGACAGCGTGGAGAGCAGCAATTAAGCTCAAG 1191
Qy 250 ArgSerPheSerLeuAspLysSerValSerValSerValSerAlaSerMetAlaAlaSerLeu 269
Db 1192 CGTTCCTTCTCTCGATATCAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTA 1251
Qy 270 HisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1252 CATGGCTTCTCTCATCAGAGATGCTTTGGAACTACTACAAACCTTCCACTACTCTGGAT 1311
Qy 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
Db 1312 GGGACCAACAGATATGCCAGTCTCTCCCTGTTTCAAGAACTATCGAGCAGACTCCCGAA 1371
Qy 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1372 ACCAGTCTGATAAGGAGGAGGAGCAGCTCCCAAGAGCTGCAGACCGCCAGGCGCTTCA 1431
Qy 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
Db 1432 GACAGCCAGGAGCAGATTCATTCGTCAGAACACAGCAGCGTGGCCAGCCCGCAGAGG 1491
Qy 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
Db 1492 TCCCTTTTATCTCACTGCATCGAAGTGGAGCGGTGGAGGACAATTAACACACAGCTTC 1551
Qy 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLys 389
Db 1552 CTTTTCGGCTTTCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1611
Qy 390 GlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrp 409
Db 1612 GGCTGGCACTCGATATCTTGGSCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGG 1671
Qy 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
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Db 1672 TATTTTGCACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGGAGGAGTGCC 1731
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Db 1732 AGTTACTCTGCTACAGCTGCAGCAGCTGCCACTTGGCGAGACCAAGTCTATTCTGTG 1791
Qy 450 ArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSer 469
Db 1792 CCACAGCGCAGAGCCAAAGTGACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGC 1851
Qy 470 PropheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489
Db 1852 CCCTTTGAAAAGCAGCTTTAAACCGCAGAGCTGCCAAATGGAAATTTGGAGAGCATCATG 1911
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 1912 TCAGAGAACAGCTCACGGGAGAGCTGGGAAAGTGGGAGTCAGTCTAGCTTTTCGGGC 1971
Qy 510 SerMetGluIleIleGluValSer 517
Db 1972 AGCATGGAATCATTGAGCTCTCC 1995

RESULT 2
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2583)
US-09-816-494-1

Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 488.00 Matches: 488
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.39% Indels: 0
DB: 4 Gaps: 0

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Qy 50 ProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlu 69
Db 1180 CCGTACTTATCCCGAGTCTCAATTCCTCGTGTGCTGTGAATGACAGCTTTTGTGAG 1239
Qy 70 LysIleLeuProThrLeuAspLysSerValAspPheIleGlyLysAlaLysAlaSerAsn 89
Db 1240 AAAATTTTGGCGTGTGGACAAATCAGTAGATTTTCATTGAGAAACAAAGCCCTCCAAAT 1299
Qy 90 GlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAla 109
Db 1300 GGATGTGTC-AGTCACTGTTAGTGGGATCTCCGCTCCGCCACCATCGCTATCGCC 1359
Qy 110 TyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLys 129
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Db 1360 TACATCATGAGGATGACATGCTTTAGATGAGCTTACAGTTTGTGAAGAAAA 1419
Qy 130 ArgProThrIleSerProAsnPhenPheLeuGlyGlnLeuLeuAspTyrGluLeuLys 149
Db 1420 AGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGACTATGAGAAG 1479
Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlu 169
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Qy 170 LysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeu 189
Db 1540 AAGCCAAATGAACCTGCTCTCTCTCAGAGGTGGACAGAAAGCGAGACGCCCTC 1599
Qy 190 SerProProCysAlaAspSerAlaThrSerGluAlaGlyGlnArgProValHisPro 209
Db 1600 AGTCCACCTGTGGCAGCTCTGCTACCTCAGAGGAGGACAAAGCCGCGTCATCC 1659
Qy 210 AlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 229
Db 1660 GCCAGCGTGCCAGCGTGCCAGCGTGCGCGCTGCTGTAGAGGACAGCCCGCTGTA 1719
Qy 230 GlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLys 249
Db 1720 CAGGCGCTCAGTGGCTGCACCTGTCGACAGACAGGCTGGAAGACAGCAATAAGCTCAAG 1779
Qy 250 ArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeu 269
Db 1780 CGTTCTCTCTCTGATATCAATCAGTTTCATATTACGCCAGCATGGCGATCTCTTA 1839
Qy 270 HisGlyPheSerSerSerGluAlaLeuGluTyrTyrLysProSerThrThrLeuAsp 289
Db 1840 CATGCGCTTCTCTCATCAGAGATGCTTTGGAATACTACAAACCTTCCACTCTGGAT 1899
Qy 290 GlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlu 309
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Qy 310 ThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSer 329
Db 1960 ACCAGTCTGTATAGAGGAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCA 2019
Qy 330 AspSerGlnSerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArg 349
Db 2020 GACAGCCAGAGCAAGCGATTGCATTCGGTCAGAACCCAGACGATGCGCCAGAGG 2079
Qy 350 SerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPhe 369
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Qy 370 LeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuLys 389
Db 2140 CTTTTGGCCCTTCCACGAGCAGCAGCACCTCAGAAAGTCTGCTGGCCCTGGCCCTTAAG 2199
Qy 390 GlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyr 409
Db 2200 GCTGCGACTCGATATCTTGCCCCCAGACCTCTATCCCTTCCCTTGACGACGCTGG 2259
Qy 410 TyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAla 429
Db 2260 TATTTTGCACAGATCTCTACATCTCTCTGCTCAGCCATCTAGCGAGCAGTGGC 2319
Qy 430 SerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerVal 449
Db 2320 AGTTACTCTGCTCAGCTCAGCGACGCTGCCACTTGGCGGAGACCAAGTCTATTCTGTG 2379
Qy 450 ArgArgArgGlnLysProSerAspAlaAspSerArgSerTyrHisGluGluSer 469
Db 2380 CGCAGCGGAGAGACCCAGTGCAGAGCTGACTCCGGCGGAGCTGGCATGAGAGAGC 2439
Qy 470 ProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMet 489

Db 2440 CCCTTTGAAGCAGCTTTAAACGAGAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATG 2499
Qy 490 SerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGly 509
Db 2500 TCAGAGAACAGCTCAGCGGAAGAGCTGGGAAAGTGGGAGTCTAGTCTAGCTTTTCGGC 2559
Qy 510 SerMetGluIleLeuGluValSer 517
Db 2560 AGCATGGAATCATTTAGGTCTCC 2583
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US-09-920-668-3
; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RTS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(2012)
US-09-920-668-3
Alignment Scores:
Pred. No.: 2,78e-10 Length: 2377
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.87% Indels: 0
Gaps: 0
US-09-964-277-21 (1-517) x US-09-920-668-3 (1-2377)
Qy 94 ValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIleMetLys 113
Db 864 GTCCACTGTCTGGTGGCATCTCCGCTCTGCCACCATGCCCATCATCATGAAG 923
RESULT 4
US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0002 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 1135:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2109 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GENBANK
;; CLONE: g1418933
US-09-016-434-1135

Alignment Scores:
Pred. No.: 0.0302 Length: 2109
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.32% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-016-434-1135 (1-2109)

Qy 92 ValLeuValHisCysLeuAlaGlyIleSerArgSer 103
Db 1216 GTCTTGGTACATTGCTTGGCTGGCATTAGCCGCTCA 1251

RESULT 5
US-09-023-655-946
; Sequence 946, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 946:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2109 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GENBANK
;; CLONE: g1418933
US-09-023-655-946

Alignment Scores:
Pred. No.: 0.0302 Length: 2109
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.32% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-023-655-946 (1-2109)

Qy 92 ValLeuValHisCysLeuAlaGlyIleSerArgSer 103
Db 1216 GTCTTGGTACATTGCTTGGCTGGCATTAGCCGCTCA 1251

RESULT 6
US-09-389-681-310/c
; Sequence 310, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 310
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (250)
; OTHER INFORMATION: n=A,T,C or G
US-09-389-681-310

Alignment Scores:
Pred. No.: 4.74 Length: 320
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-389-681-310 (1-320)

Qy 98 AlaGlyIleSerArgSerAlaThrIle 106
Db 74 GCAGGCAATTTCCCGTCCAGCCACCATC 48

RESULT 7
US-09-620-405B-310/c
; Sequence 310, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun

APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C8
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 310
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (250)
OTHER INFORMATION: n=A,T,C or G
US-09-620-405B-310

Alignment Scores:
Pred. No.: 4.74 Length: 320
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-620-405B-310 (1-320)

QY 98 AlaglyleSerArgSerAlaThrIle 106
Db 74 GCAGGCATTTCCTCCGTCAGCCACCATC 48

RESULT 8
US-09-339-338-310/c
Sequence 310, Application US/09339338A
Patent No. 6573368
GENERAL INFORMATION:
APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C2
CURRENT APPLICATION NUMBER: US/09/339,338A
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 310
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (250)
OTHER INFORMATION: n=A,T,C or G
US-09-339-338-310

Alignment Scores:
Pred. No.: 4.74 Length: 320
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-339-338-310 (1-320)

QY 98 AlaglyleSerArgSerAlaThrIle 106
Db 74 GCAGGCATTTCCTCCGTCAGCCACCATC 48

RESULT 9
US-09-433-826B-310/c
Sequence 310, Application US/09433826B
Patent No. 6579973
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433,826B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 474
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 310
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (250)
OTHER INFORMATION: n=A,T,C or G
US-09-433-826B-310

Alignment Scores:
Pred. No.: 4.74 Length: 320
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-433-826B-310 (1-320)

QY 98 AlaglyleSerArgSerAlaThrIle 106
Db 74 GCAGGCATTTCCTCCGTCAGCCACCATC 48

RESULT 10
US-09-604-287A-310/c
Sequence 310, Application US/09604287A
Patent No. 6586572
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 310
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (250)
OTHER INFORMATION: n=A,T,C or G
US-09-604-287A-310

Alignment Scores:
Pred. No.: 4.74 Length: 320
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-604-287A-310 (1-320)

Qy 98 AlaGlyIleSerArgSerAlaThrIle 106
Db 74 GCAGGCATTTCCCGGTCCAGCCACATC 48

RESULT 11

US-09-834-759-310/c
; Sequence 310, Application US/09834759
; Patent No. 6580197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 310
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (250)
; OTHER INFORMATION: n=A,T,C or G
US-09-834-759-310

Alignment Scores:
Pred. No.: 4.74 Length: 320
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-834-759-310 (1-320)

Qy 98 AlaGlyIleSerArgSerAlaThrIle 106
Db 74 GCAGGCATTTCCCGGTCCAGCCACATC 48

RESULT 12

US-09-389-681-311/c
; Sequence 311, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-389-681-311

Alignment Scores:
Pred. No.: 8.08 Length: 539
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-389-681-311 (1-539)

Qy 98 AlaGlyIleSerArgSerAlaThrIle 106
Db 136 GCAGGCATTTCCCGGTCCAGCCACATC 110

RESULT 13

US-09-620-405B-311/c
; Sequence 311, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-311

Alignment Scores:
Pred. No.: 8.08 Length: 539
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.74% Indels: 0
DB: 4 Gaps: 0

US-09-964-277-21 (1-517) x US-09-620-405B-311 (1-539)

Qy 98 AlaGlyIleSerArgSerAlaThrIle 106
Db 136 GCAGGCATTTCCCGGTCCAGCCACATC 110

RESULT 14

US-09-339-338-311/c
; Sequence 311, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 539
; TYPE: DNA

```

; ORGANISM: Homo sapiens
US-09-339-338-311

Alignment Scores:
Pred. No.:      8.08      Length:      539
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      1.74%      Indels: 0
DB:              4      Gaps: 0

US-09-964-277-21 (1-517) x US-09-339-338-311 (1-539)

QY 98 AlaGlylleSerArgSerAlaThrIle 106
DB 136 GCAGGCATTCCCGGTGAGCCACCATC 110

RESULT 15
US-09-433-826B-311/c
; Sequence 311, Application US/09433826B
; Patent No. 6579873
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-311

Alignment Scores:
Pred. No.:      8.08      Length:      539
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      1.74%      Indels: 0
DB:              4      Gaps: 0

US-09-964-277-21 (1-517) x US-09-433-826B-311 (1-539)

QY 98 AlaGlylleSerArgSerAlaThrIle 106
DB 136 GCAGGCATTCCCGGTGAGCCACCATC 110

Search completed: February 28, 2004, 04:14:26
Job time : 117 secs
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